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OM protein - protein search, using sw model

Run on: September 23, 2003, 15:09:23 ; Search time 45 Seconds
(without alignments)
821.851 Million cell updates/sec

Title: US-09-909-005-1

Perfect score: 1170

Sequence: 1 MLKPSVTSAPTADMTLVV.....LLIQQQQQQQQQTQQNHMS 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_19Jun03.*

1: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1170	100.0	233	20 AAY29978	Human cell junctio
2	1170	100.0	233	22 AAU07127	Human cell junctio
3	1170	100.0	233	23 AAU93326	Human cell junctio
4	814	69.6	197	22 AAM78892	Human protein sequ
5	814	69.6	197	22 AAB93600	Human protein sequ
6	814	69.6	198	22 AAM79876	Human protein sequ
7	807	69.0	207	22 AAE03655	Human extracellular
8	807	69.0	207	22 AAU93629	Human PRO protein,
9	754	64.4	195	22 ABB63428	Drosophila melanog

10	669	57.2	167	22	AAU17388	Novel signal trans
11	579	49.5	163	22	AAU17399	Novel signal trans
12	575	49.1	150	21	AAB43364	Human ORFX ORF3128
13	472	40.3	97	22	AAB55836	PDZ encoded domain
14	472	40.3	97	22	AAB57627	Tax interaction pr
15	472	40.3	97	22	AAB58037	Tax interaction pr
16	472	40.3	97	22	ABJ05302	PDZ domain protein
17	467	39.9	91	23	ABP63172	TAX-IP 33 PDZ doma
18	208.5	17.8	960	22	ABB58434	Drosophila melanog
19	203.5	17.4	817	19	AAW48101	Human discs large
20	203.5	17.4	817	20	AAJ30137	Human acid sequenc
21	203.5	17.4	849	19	AAW48102	Human discs large
22	197.5	16.9	882	18	AAW34662	Partial PSD-93 pro
23	196.5	16.8	724	23	ABB04798	LDL receptor bindi
24	196.5	16.8	767	23	ABP65167	Hypoxia-regulated
25	196.5	16.8	767	23	AAU84269	Human endometrial
26	196.5	16.8	767	23	AAU84328	Protein DLG4 diffe
27	194.5	16.6	767	21	AAJ22138	Human post-synapti
28	190.5	16.3	85	23	AAU87939	Human PDZ domain #
29	190	16.2	1881	20	AAJ24025	Amino acid sequenc
30	181.5	15.5	344	22	AAB55834	PDZ encoded domain
31	181.5	15.5	344	22	AAB57623	Human post-synapti
32	181.5	15.5	344	22	AAB58035	Human post-synapti
33	181.5	15.5	344	23	ABJ05300	PDZ domain protein
34	180.5	15.4	338	23	ABP63160	Human PSD95 PDZ do
35	180.5	15.4	442	23	ABP63536	Human PSD95 PDZ do
36	180.5	15.4	724	23	ABB04807	LDL receptor bindi
37	180.5	15.4	2466	16	AAU71498	Human protein tyro
38	180.5	15.4	2466	19	AAU75999	Intracellular phosph
39	180.5	15.4	2466	21	AAJ90272	Human PrPL1 phosph
40	176.5	15.1	763	20	AAJ04731	PDZ domain-contain
41	176.5	15.1	1005	20	AAJ04731	Mature protein con
42	176.5	15.1	1373	20	AAJ04730	Protein containing
43	176.5	15.1	2000	20	AAJ04732	Protein containing
44	176.5	15.1	2070	20	AAJ04733	Protein containing
45	174.5	14.9	304	22	AAM93296	Human polypeptide,

ALIGNMENTS

RESULT 1
AAY29978
ID AAY29978 standard; Protein; 233 AA.
XX
AC AAY29978;
XX
DT 23-NOV-1999 (first entry)
XX
DE Human cell junction PDZ protein CJPDPZ.
XX
DE Human; cell junction PDZ protein; PDZ domain; CJPDPZ; diagnosis;
KW cancer; neurological disorder; developmental disorder;
KW William's syndrome.
XX
OS Homo sapiens.
XX
PN US5958731-A.
XX
PD 28-SEP-1999.
XX
PF 11-SEP-1998; 98US-0151611.
XX
PR 11-SEP-1998; 98US-0151611.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Yue H, Patterson C, Au-Young J;
XX
DR WPI: 1999-561035/47.
DR N-FSDB; AA221259.
XX
PT Nucleic acids encoding cellular junction PDZ protein domains useful in

PT the prevention, diagnosis and treatment of disorders associated with
 PT defective cell signalling such as cancers and neurological and
 XX developmental disorders -

PS Claim 1; Column 39-40; 27pp; English.

XX The present sequence represents human cell junction PDZ protein (CJPDZ).
 CC CJPDZ polynucleotides and proteins may be used in the diagnosis,
 CC prevention and treatment of disorders associated with defective cell
 CC signalling. They may be used to treat cancers, neurological disorders
 CC and developmental disorders such as William's syndrome. CJPDZ or vectors
 CC containing CJPDZ may be administered to treat any of the above diseases
 CC by rectifying mutations or deletions in a patient's genome that affect
 CC cell signalling by expressing inactive proteins or to supplement the
 CC patients own production of CJPDZ protein domains. Antisense nucleic acid
 CC molecules may be administered to down regulate CJPDZ protein domain
 CC expression by binding with the cells own CJPDZ genes and preventing
 CC their expression. CJPDZ polynucleotides may also be used as DNA probes
 CC in diagnostic assays to detect and quantitate the presence of similar
 CC nucleic acid sequences in samples, and hence which patients may be in
 CC need of restorative therapy. They may also be used to study the
 CC expression and function of CJPDZ protein domains and their role in
 CC cellular signalling. The CJPDZ protein domains may be used as antigens
 CC in the production of antibodies and in assays to identify modulators
 CC of CJPDZ expression and activity.

XX SQ Sequence 233 AA;

Query Match 100.0%; Score 1170; DB 20; Length 233;
 Best Local Similarity 100.0%; Pred. No. 3.3e-108;
 Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKPSVTSAPTADMATLVVQPLTDRDVARAIELLEKLOESGVPVHKLSLKKVLQSE 60
 Db 1 MKPSVTSAPTADMATLVVQPLTDRDVARAIELLEKLOESGVPVHKLSLKKVLQSE 60

Qy 61 FCTAIRVYQYMHETITVNGCPEFRARATATVAATAAASGSHSPRVVLPKTDGLGF 120
 Db 61 FCTAIRVYQYMHETITVNGCPEFRARATATVAATAAASGSHSPRVVLPKTDGLGF 120

Qy 121 NVMGKEQNSPIYISRIIPGGVAERHGLKRGDQLLSVNGSVSVEGHEHKAVELLKAAD 180
 Db 121 NVMGKEQNSPIYISRIIPGGVAERHGLKRGDQLLSVNGSVSVEGHEHKAVELLKAAD 180

Qy 181 SVKLIVRYTPKVLMEARFEKLTARRRQOQLLIQOQQOQQOQQOQQOQHMS 233
 Db 181 SVKLIVRYTPKVLMEARFEKLTARRRQOQLLIQOQQOQQOQQOQQOQHMS 233

RESULT 2

AAU07127
 ID AAU07127 standard; Protein; 233 AA.

XX AC AAU07127;

XX 24-OCT-2001 (first entry)

XX Human cell junction PDZ protein, CJPDZ.

XX Human; cell junction PDZ protein; CJPDZ; antigen; antibody; cytostatic;
 KW anti-leukaemic; neuroprotective; antiepileptic; anti-Alzheimer's disease;
 KW neurotropic; anti-convulsant; cancer; leukaemia; myeloma; sarcoma;
 KW neurological disorder; epilepsy; Alzheimer's disease;
 KW Huntington's chorea.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Domain 107..189

XX /label= PDZ_domain

XX US6265547-B1.

XX

PD 24-JUL-2001.

XX 06-AUG-1999; 99US-0370102.

XX 11-SEP-1998; 98US-0151611.

XX (INCYTE) INCYTE GENOMICS INC.

XX Yue H, Au-young J, Patterson C;

XX WPI; 2001-463943/50.

XX N-ESDB; AAS11583.

XX Cellular junction PDZ proteins useful in the prevention, diagnosis and
 PT treatment of disorders associated with defective cell signalling such as
 PT cancers, neurological disorders and developmental disorders such as
 PT William's syndrome -

PS Claim 1; Fig 1; 28pp; English.

XX The invention relates to a purified human cell junction PDZ (CJPDZ)
 CC polypeptide. The polypeptide may be used as an antigen in the production
 CC of antibodies against CJPDZ and in assays to identify molecules
 CC which bind CJPDZ including modulators of CJPDZ expression and activity.
 CC The anti-CJPDZ antibodies, agonists and antagonists may be used to
 CC control/regulate expression and activity of CJPDZ. The anti-CJPDZ
 CC antibodies may also be used as diagnostic agents for detecting the
 CC presence of CJPDZ polypeptides in samples (e.g. by enzyme linked
 CC immunosorbent assay, ELISA). Disorders of cell signalling and CJPDZ
 CC expression and activity that may be prevented, diagnosed and/or treated
 CC by the above methods include, for example cancers (e.g. leukaemia,
 CC myeloma, sarcoma or lung, liver, colon or spleen cancer), neurological
 CC disorders (e.g. epilepsy, Alzheimer's disease and/or Huntington's
 CC chorea). A full list of disorders that may be treated is given in the
 CC specification. The present sequence represents human CJPDZ.

XX SQ Sequence 233 AA;

Query Match 100.0%; Score 1170; DB 22; Length 233;
 Best Local Similarity 100.0%; Pred. No. 3.3e-108;
 Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKPSVTSAPTADMATLVVQPLTDRDVARAIELLEKLOESGVPVHKLSLKKVLQSE 60
 Db 1 MKPSVTSAPTADMATLVVQPLTDRDVARAIELLEKLOESGVPVHKLSLKKVLQSE 60

Qy 61 FCTAIRVYQYMHETITVNGCPEFRARATATVAATAAASGSHSPRVVLPKTDGLGF 120
 Db 61 FCTAIRVYQYMHETITVNGCPEFRARATATVAATAAASGSHSPRVVLPKTDGLGF 120

Qy 121 NVMGKEQNSPIYISRIIPGGVAERHGLKRGDQLLSVNGSVSVEGHEHKAVELLKAAD 180
 Db 121 NVMGKEQNSPIYISRIIPGGVAERHGLKRGDQLLSVNGSVSVEGHEHKAVELLKAAD 180

Qy 181 SVKLIVRYTPKVLMEARFEKLTARRRQOQLLIQOQQOQQOQQOQQOQHMS 233
 Db 181 SVKLIVRYTPKVLMEARFEKLTARRRQOQLLIQOQQOQQOQQOQQOQHMS 233

RESULT 3

AAU99326

ID AAU99326 standard; Protein; 233 AA.

XX AC AAU99326;

XX 07-OCT-2002 (first entry)

XX Human cell junction PDZ (CJPDZ) protein.

XX Human; cytostatic; neurotropic; neuroprotective; endocrine;

XX cell junction PDZ; CJPDZ; membrane-associated signalling protein;

XX signal transduction; postsynaptic density protein 95; PSD-95;

XX Drosophila lethal (1) discs large-1; Dig; zonula occludens-1; ZO-1;

Db 6 EPVRLERDICRAIELLEKQSGEVPVPPQKLAQALQRLQSEFCNAYREVYEHVETVDISS 65
 QY 81 CPEFRARATATVAATAFAASGSHGSHPRVVELPKTDGELGFNVMGKEQNSPIYISRIIPG 140
 Db 66 SPEVRANATATVAATAFAASGSHGSHPRVVELPKTEEGLGFNMGKEQNSPIYISRIIPG 125
 QY 141 GVAERHGLKRGDQLLSVNGSVSGEHEHEKAVELLKAAKDSVKLVVRYTPKVLMEARF 200
 Db 126 GIADRHGGLKRGDQLLSVNGSVSGEHEHEKAVELLKAAQGVKLVVRYTPKVLMEESRF 185
 QY 201 EKLRTARRRQ 211
 Db 186 EKMSAKRRQ 196

RESULT 5
 AAB93600
 ID AAB93600 standard; Protein; 197 AA.
 AC AAB93600;
 XX 26-JUN-2001 (first entry)
 DE Human protein sequence SEQ ID NO:13038.
 XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.
 KW Homo sapiens.
 OS
 PN EP1074617-A2.
 XX 07-FEB-2001.
 PD 28-JUL-2000; 2000EP-0116126.
 PF 29-JUL-1999; 99JP-0248036.
 PR 27-AUG-1999; 99JP-0300253.
 PR 11-JAN-2000; 2000JP-0118776.
 PR 02-MAY-2000; 2000JP-0183767.
 PR 09-JUN-2000; 2000JP-0241899.
 XX (HELI-) HELIX RES INST.
 PA Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX WPI; 2001-318749/34.
 XX Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX Claim 8; SEQ ID 13038; 2537pp + CD ROM; English.
 PS The present invention describes primer sets for synthesising 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesising polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and

CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 XX Sequence 197 AA;
 SQ Query Match 69.6%; Score 814; DB 22; Length 197;
 Best Local Similarity 80.6%; Pred. No. 8e-73;
 Matches 154; Conservative 24; Mismatches 13; Indels 0; Gaps 0;
 QY 21 QPLTLDRDVARAIELLEKIQSGEVPVHKLQSLKVLQSEFCTATREYVOYMHETVNG 80
 Db 6 EPVRLERDICRAIELLEKQSGEVPVPPQKLAQALQRLQSEFCNAYREVYEHVETVDISS 65
 QY 81 CPEFRARATATVAATAFAASGSHGSHPRVVELPKTDGELGFNVMGKEQNSPIYISRIIPG 140
 Db 66 SPEVRANATATVAATAFAASGSHGSHPRVVELPKTEEGLGFNMGKEQNSPIYISRIIPG 125
 QY 141 GVAERHGLKRGDQLLSVNGSVSGEHEHEKAVELLKAAKDSVKLVVRYTPKVLMEARF 200
 Db 126 GIADRHGGLKRGDQLLSVNGSVSGEHEHEKAVELLKAAQGVKLVVRYTPKVLMEESRF 185
 QY 201 EKLRTARRRQ 211
 Db 186 EKMSAKRRQ 196

RESULT 6
 AAM79876
 ID AAM79876 standard; Protein; 198 AA.
 AC AAM79876;
 XX 06-NOV-2001 (first entry)
 DE Human protein SEQ ID NO 3522.
 XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 XX Homo sapiens.
 OS
 PN WO200157190-A2.
 XX 09-AUG-2001.
 PD 05-FEB-2001; 2001WO-US04098.
 PF 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 PR 20-JUN-2000; 2000US-0598075.
 PR 19-JUL-2000; 2000US-0620325.
 PR 01-SEP-2000; 2000US-0654936.
 PR 15-SEP-2000; 2000US-0663561.
 PR 20-OCT-2000; 2000US-0693325.
 PR 30-NOV-2000; 2000US-0728422.
 XX (HYSE-) HYSEQ INC.
 PA Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
 PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX WPI; 2001-476283/51.
 DR N-PSDB; AAK53009.
 XX Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -
 XX Claim 20; Page 370; 622pp; English.

RESULT 8
AAU83629
ID AAU83629 standard; Protein; 207 AA.
XX AC AAU83629;
XX DT 08-MAY-2002 (first entry)
XX DE Human PRO protein, Seq ID No 76.
XX DE Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha.
XX OS Homo sapiens.
XX PN WO200208288-A2.
XX PD 31-JAN-2002.
XX PF 29-JUN-2001; 2001WO-US21066.
XX PR 20-JUL-2000; 2000US-219556P.
XX PR 25-JUL-2000; 2000US-220583P.
XX PR 25-JUL-2000; 2000US-220603P.
XX PR 25-JUL-2000; 2000US-220607P.
XX PR 25-JUL-2000; 2000US-220624P.
XX PR 25-JUL-2000; 2000US-220638P.
XX PR 25-JUL-2000; 2000US-220664P.
XX PR 25-JUL-2000; 2000US-220666P.
XX PR 26-JUL-2000; 2000US-220893P.
XX PR 28-JUL-2000; 2000WO-US20710.
XX PR 23-AUG-2000; 2000WO-US23522.
XX PR 24-AUG-2000; 2000WO-US23328.
XX PR 15-SEP-2000; 2000US-000000P.
XX PR 10-NOV-2000; 2000WO-US30873.
XX PR 28-NOV-2000; 2000US-253646P.
XX PR 01-DEC-2000; 2000WO-US32678.
XX PR 20-DEC-2000; 2000US-0747259.
XX PR 20-DEC-2000; 2000WO-US34956.
XX PR 28-FEB-2001; 2001WO-US06520.
XX PR 10-MAY-2001; 2001US-0854280.
XX PR 25-MAY-2001; 2001WO-US17092.
XX PA (GETH) GENENTECH INC.
XX PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX WPI; 2002-172001/22.
XX DR N-PSDB; ABK33573.
XX PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
XX PT useful for treating a PRO related disorder and for diagnosing tumours
XX PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
XX PT tumour or liver tumour -
XX PS Claim 11; Figure 76; 359pp; English.
XX CC The invention relates to one hundred and twenty two nucleic acids
XX CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
XX CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
XX CC agonists and antagonists are useful for treating a PRO related disorder.
XX CC The PRO polypeptides are useful for diagnosing tumours, especially lung
XX CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
XX CC liver tumour. The PRO polypeptides are useful for stimulating the
XX CC proliferation of, or gene expression, in pericyte cells, for stimulating
XX CC the proliferation or differentiation of chondrocyte cells, for
XX CC stimulating the release of tumour necrosis factor-alpha from human blood,
XX CC for stimulating or inhibiting the proliferation of normal human dermal
XX CC fibroblast cells. The PRO polypeptide may also be used as molecular

CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
CC protein sequences of the invention.
XX SQ Sequence 207 AA;
Query Match 69.0%; Score 807; DB 23; Length 207;
Best Local Similarity 78.5%; Pred. No. 4.3e-72;
Matches 157; Conservative 24; Mismatches 17; Indels 2; Gaps 1;
Qy 14 MATLVVQPLTDRVARAIELLEKLQESGVPVHKLSQKLVLOSFEFTAIREVYQMH 73
Db 1 MAAL--VEPLGLERDVSRAVELLERLQSGELPPQKLQALQVLRQSFCSAIREVYEQLY 58
Qy 74 ETITVNGCPFRARATATAKATVAFAASEGHSHPRVLPKTDGELGFNMVGKQNSPIY 133
Db 59 DTLDTGSAEIRAHATAKAIVAAFTASEGHAHPRVVELPKTDGELGFNMVGKQNSPIY 118
Qy 134 ISRIIPGGVAERHGGKRGDOLLSVNGSVSEGEHKAVALLEKAAKDSVKLVRYTPKVL 193
Db 119 ISRVIPGGVADRHGGKRGDOLLSVNGSVSEGEHKAVALLEKAAQSGVKLVRYTPRVL 178
Qy 194 EEMEARPEKLETRARRQQQ 213
Db 179 EEMEARPEKMSARRRQQHQ 198
RESULT 9
ABB63428
ID ABB63428 standard; Protein; 195 AA.
XX AC ABB63428;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 17076.
XX DE Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US09231.
XX PR 23-MAR-2000; 2000US-191637P.
XX PR 11-JUL-2000; 2000US-0614150.
XX PA (PEKE) PE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX DR N-PSDB; ABL07531.
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX PT interactions -
XX PS Disclosure; SEQ ID NO 17076; 21pp + Sequence Listing; English.
XX CC The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX CC sequences (ABL01840-ABL16175) and the encoded proteins
XX CC (ABB57737-ABB72072).

PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225266.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226868.
 PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 08-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
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 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
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 PR 14-SEP-2000; 2000US-0232398.
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 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
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 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
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 PR 29-SEP-2000; 2000US-0236370.
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 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244517.
 PR 08-NOV-2000; 2000US-0246474.

PR 08-NOV-2000; 2000US-0246475.
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 PR 08-NOV-2000; 2000US-0246478.
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 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
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 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
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 PR 17-NOV-2000; 2000US-0249217.
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 PR 17-NOV-2000; 2000US-0249244.
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 PR 17-NOV-2000; 2000US-0249297.
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 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-465460/50.

N-PSDB; AAS27316.

Novel polypeptides useful for diagnosing, treating, preventing and/or
 PT proposing disorders related to the proteins, including cancers, immune
 PT disorders and neuronal disorders -

PS Claim 1; SEQ ID No 964; 880pp; English.

CC The invention relates to novel isolated polypeptides (I), and
 CC polynucleotides (II). (I), (II) and the antibody to (I) are useful for
 CC diagnosing, preventing and treating diseases including immune system
 CC disorders (e.g. congenital and acquired immunodeficiencies, autoimmune
 CC disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ
 CC transplant rejections and graft versus host disease, infectious diseases
 CC (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and
 CC other blood-related disorders (sickle cell anaemia), myeloproliferative
 CC disorders, primary haematopoietic disorders, hyperproliferative
 CC disorders (e.g. Gaucher's disease and cancer), neurodegenerative
 CC disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal
 CC abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal

CC disorders (e.g. glomerulonephritis), cardiovascular disorders
 CC (e.g. arrhythmia), respiratory disorders, dermatological disorders, in
 CC wound healing, epithelial cell proliferation, endocrine disorders (e.g.
 CC Addison's disease), reproductive system disorders, gastrointestinal
 CC disorder (inflammatory disorders), liver disorders (cirrhosis),
 CC as stimulators of B-cell responsiveness to pathogens, activators of
 CC T-cells, to induce higher affinity antibodies, and as a means to induce
 CC tumour proliferation in pathologies e.g. acquired immune deficiency
 CC syndrome (AIDS). AAU17059-AAU17683 represent novel signal transduction
 CC pathway protein, amino acid sequences of the invention.

Query Match 49.5%; Score 579; DB 22; Length 163;
 Best Local Similarity 84.1%; Pred. No. 1.6e-49;
 Matches 111; Conservative 13; Mismatches 8; Indels 0; Gaps 0;
 QY 82 PFRARAKATVAFAASEGSHPRVVELPKTDGLGFNVMGKEQNSPIYISRIIPGG 141
 DB 23 PHQLSLSQATVAFAASEGSHPRVVELPKTDGLGFNVMGKEQNSPIYISRIIPGG 82
 QY 142 VAERHGGKRGDQLLSVNGSVSGEHEKAVELLKAAKDSVKLVVRYTPKVLMEARFE 201
 DB 83 VADRHGGKRGDQLLSVNGSVSGEHEKAVELLKAAKDSVKLVVRYTPKVLMEARFE 142
 QY 202 KLTARRRQQQ 213
 DB 143 KMSRRRRQQHQ 154

RESULT 12

AA43364
 ID AAB43364 standard; Protein; 150 AA.

AC AAB43364;

DT 08-FEB-2001 (first entry)

DE Human ORFX ORF3128 polypeptide sequence SEQ ID NO:6256.

KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
 KW vulnary; antipsoriatic; antiparkinsonian; neurotropic; neuroprotective;
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotrophic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antihypertensive;
 KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
 KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
 KW thrombosis; contraceptive.

OS Homo sapiens.

PN WO200058473-A2.

PD 05-OCT-2000.

PF 31-MAR-2000; 2000WO-US08621.

PR 31-MAR-1999; 99US-0127607.

PR 02-APR-1999; 99US-0127636.

PR 30-MAR-2000; 99US-0127728.

PR 30-MAR-2000; 2000US-0540763.

PA (CURA-) CURAGEN CORP.

PI Shinkets RA, Leach M;

XX WPI; 2000-602362/57.

DR N-PSDB; AAC7573.

XX

PT Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -

PS Claim 11; Page 5443; 5507pp; English.

XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
 CC antipsoriatic; antiparkinsonian; neurotropic; neuroprotective;
 CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotrophic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
 CC antithyroid; and antianemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.

XX Sequence 150 AA;

Query Match 49.1%; Score 575; DB 21; Length 150;
 Best Local Similarity 90.2%; Pred. No. 3.6e-49;
 Matches 111; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

QY 91 KATVAFAASEGSHPRVVELPKTDGLGFNVMGKEQNSPIYISRIIPGGVAERHGGK 150
 DB 19 KATVAFAASEGSHPRVVELPKTDGLGFNVMGKEQNSPIYISRIIPGGVADRHGGK 78

QY 151 RGDQLLSVNGSVSGEHEKAVELLKAAKDSVKLVVRYTPKVLMEARFEKLTARRRQ 210
 DB 79 RGDQLLSVNGSVSGEHEKAVELLKAAKDSVKLVVRYTPKVLMEARFEKLTARRRQ 138

QY 211 QQQ 213

DB 139 QHQ 141

RESULT 13

AA55836

ID AAB55836 standard; Peptide; 97 AA.

AC AAB55836;

XX 07-MAR-2001 (first entry)

DT PDZ encoded domain #6.

KW Hematopoietic cell; PDZ; PL; autoimmune disease; inflammation;
 KW allergy; asthma; multiple sclerosis; cancer; infection.

OS Synthetic.

PN WO200069896-A2.

PD 23-NOV-2000.

XX 12-MAY-2000; 2000WO-US13161.

XX 14-MAY-1999; 99US-0134114.

XX 14-MAY-1999; 99US-0134117.

XX 14-MAY-1999; 99US-0134118.

XX 21-OCT-1999; 99US-0160860.

PR 29-OCT-1999; 99US-0162498.
 PR 13-DEC-1999; 99US-0170453.
 PR 14-JAN-2000; 2000US-0176195.
 PR 14-FEB-2000; 2000US-0182296.
 PR 11-APR-2000; 2000US-0196460.
 PR 11-APR-2000; 2000US-0196527.
 XX (ARBO-) ARBOR VITA CORP.
 XX
 XX Lu PS;
 PI WPI; 2001-080245/09.
 DR
 XX

Modulating a biological function of an endothelial cell or hematopoietic cell, useful for treating autoimmune diseases and infectious diseases, by administering an antagonist that inhibits binding between a PDZ protein and a PL protein -

XX Disclosure; Page 28-43; 141pp; English.

XX The present invention relates to a new method for modulating a biological function of an endothelial cell or hematopoietic cell. The method involves introducing into a cell, an antagonist that inhibits binding between a PDZ protein and a PL protein. The inhibitor is used to treat a disease mediated by hematopoietic cells, e.g. autoimmune disease. It may also be used to prevent transplantation rejection of a solid organ transplant. The method may also be used in the treatment of inflammation, allergy, inflammatory bowel diseases, ulcerative colitis, ileitis, psoriasis, asthma, atopic dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis, graft rejection, transplantation rejection), atherosclerosis, cancers, infectious diseases, ischemia, vasculitis and Crohn's disease.

XX Sequence 97 AA;

Query Match 40.3%; Score 472; DB 22; Length 97;

Best Local Similarity 100.0%; Pred. No. 3.6e-39;

Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 HSHPRVVELPKTDEGLGFNMVGKEQNSPIYISRIIPGGVAERHGLKRGDQLLSYNGVS 162

Db 1 HSHPRVVELPKTDEGLGFNMVGKEQNSPIYISRIIPGGVAERHGLKRGDQLLSYNGVS 60

QY 163 VEGEHKAVELLKAAKDSVKLVRYTPKYLE 194

Db 61 VEGEHKAVELLKAAKDSVKLVRYTPKYLE 92

RESULT 14

AAB57627

ID AAB57627 standard; Protein; 97 AA.

XX

AC AAB57627;

XX

DT 12-MAR-2001 (first entry)

XX

DE Tax interaction protein 33 PDZ domain.

XX

KW Endothelial cell; hematopoietic cell; PDZ domain protein;

KW PL domain protein; leukocyte activation; synapse formation;

KW transmembrane neurotransmitter receptor; autoimmune disease;

KW transplantation rejection; inflammation; allergy;

KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;

KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;

KW ischaemia; vasculitis; Crohn's disease.

XX Homo sapiens.

XX OS

XX WO200069897-A2.

XX

XX 23-NOV-2000.

XX

PF 12-MAY-2000; 2000WO-US13166.
 XX
 PR 14-MAY-1999; 99US-0134114.
 PR 14-MAY-1999; 99US-0134117.
 PR 14-MAY-1999; 99US-0134118.
 PR 21-OCT-1999; 99US-0160860.
 PR 29-OCT-1999; 99US-0162498.
 PR 13-DEC-1999; 99US-0170453.
 PR 14-JAN-2000; 2000US-0176195.
 PR 14-FEB-2000; 2000US-0182296.
 PR 11-APR-2000; 2000US-0196460.
 PR 11-APR-2000; 2000US-0196527.
 XX (ARBO-) ARBOR VITA CORP.
 XX
 XX Lu PS;
 PI WPI; 2001-025003/03.
 DR
 XX

New inhibitors of binding of a PDZ protein and PL protein for

inhibiting T cell-mediated response by hematopoietic cells, or for treating diseases characterized by inflammatory and humoral immune responses, e.g. inflammation, cancer -

XX Disclosure; Page 30; 139pp; English.

XX The present invention relates to a method for modulating a biological function of an endothelial cell or hematopoietic cell, comprises introducing into a cell an antagonist that inhibits binding between a PDZ domain protein and a PL domain protein to result in inhibition of leukocyte activation. The present sequence is a PDZ domain. PDZ domains of proteins are named after three prototypical proteins: PSD95, Drosophila large disc protein and Zonula Occludin 1 protein. PDZ domain proteins are involved in synapse formation by organising transmembrane neurotransmitter receptors through intracellular interactions. The inhibitors identified by the present invention can be used to treat a disease mediated by hematopoietic cells, e.g. autoimmune disease, inflammation, allergy (e.g. drug allergies), inflammatory bowel diseases, ulcerative colitis, ileitis, psoriasis, respiratory allergic diseases (e.g. asthma), atopic dermatitis, autoimmune diseases (e.g. rheumatoid arthritis, multiple sclerosis, insulin-dependent diabetes, Hashimoto thyroiditis, osteoarthritis), atherosclerosis, cancers, infectious diseases (e.g. viral infection), ischaemia, vasculitis and Crohn's disease. The inhibitors can also be used to prevent transplantation rejection of a solid organ transplant.

XX Sequence 97 AA;

Query Match 40.3%; Score 472; DB 22; Length 97;

Best Local Similarity 100.0%; Pred. No. 3.6e-39;

Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 HSHPRVVELPKTDEGLGFNMVGKEQNSPIYISRIIPGGVAERHGLKRGDQLLSYNGVS 162

Db 1 HSHPRVVELPKTDEGLGFNMVGKEQNSPIYISRIIPGGVAERHGLKRGDQLLSYNGVS 60

QY 163 VEGEHKAVELLKAAKDSVKLVRYTPKYLE 194

Db 61 VEGEHKAVELLKAAKDSVKLVRYTPKYLE 92

RESULT 15

AAB58037

ID AAB58037 standard; Protein; 97 AA.

XX AAB58037;

AC

XX 12-MAR-2001 (first entry)

XX

XX Tax interaction protein 33 PDZ domain.

DE

XX Endothelial cell; hematopoietic cell; PDZ domain protein;

KW PL domain protein; leukocyte activation; synapse formation;

KW

KW transmembrane neurotransmitter receptor; autoimmune disease;
KW transplantation rejection; inflammation; allergy;
KW inflammatory bowel disease; ulcerative colitis; ileitis; psoriasis;
KW asthma; atopic dermatitis; atherosclerosis; cancer; infectious disease;
KW ischaemia; vasculitis; Crohn's disease.

XX Homo sapiens.

OS WO200069898-A2.

XX 23-NOV-2000.

PD 12-MAY-2000; 2000WO-US13205.

XX 14-MAY-1999; 99US-0134114.

PR 14-MAY-1999; 99US-0134117.

PR 14-MAY-1999; 99US-0134118.

PR 21-OCT-1999; 99US-0160860.

PR 29-OCT-1999; 99US-0162498.

PR 13-DEC-1999; 99US-0170453.

PR 14-JAN-2000; 2000US-0176195.

PR 14-FEB-2000; 2000US-0182296.

PR 11-APR-2000; 2000US-0196460.

PR 11-APR-2000; 2000US-0196527.

XX (ARBO-) ARBOR VITA CORP.

PA Lu PS;

PI WPI; 2001-061214/07.

DR Modulating a biological function of a hematopoietic cell for treating

XX an allergic response, or diseases mediated by immune system cells,

PT comprises introducing into the cell a PDZ-PL interaction enhancer or

PT inhibitor.

PS Disclosure; Page 32; 143pp; English.

XX The present invention relates to a method for modulating a biological
CC function of an endothelial cell or haematopoietic cell, comprises
CC introducing into a cell an antagonist that inhibits binding between a
CC PDZ domain protein and a PL domain protein to result in inhibition of
CC leukocyte activation. The present sequence is a PDZ domain. PDZ domains
CC of proteins are named after three prototypical proteins: PSD95,
CC Drosophila large disc protein and Zonula Occludin 1 protein. PDZ domain
CC neurotransmitter receptors through intracellular interactions. The
CC inhibitors identified by the present invention can be used to treat a
CC disease mediated by haematopoietic cells, e.g. autoimmune disease,
CC inflammation, allergy (e.g. drug allergies), inflammatory bowel diseases,
CC ulcerative colitis, ileitis, psoriasis, respiratory allergic diseases
CC (e.g. asthma), atopic dermatitis, autoimmune diseases (e.g. rheumatoid
CC arthritis, multiple sclerosis, insulin-dependent diabetes, Hashimoto
CC thyroiditis, osteoarthritis), atherosclerosis, cancers, infectious
CC diseases (e.g. viral infection), ischaemia, vasculitis and Crohn's
CC disease. The inhibitors can also be used to prevent transplantation
CC rejection of a solid organ transplant.

XX Sequence 97 AA;

Query Match 40.3%; Score 472; DB 22; Length 97;
Best Local Similarity 100.0%; Pred. No. 3.6e-39;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 HSHPRVVELPKTDEGLGFNVNMGKEQNSPIYISRIIPGVVAERHGLKRGDQLLSVNGVS 60
QY 163 VEGEHHEKAVELLKAADSVKLVVRYTPKYLE 194
Db 61 VEGEHHEKAVELLKAADSVKLVVRYTPKYLE 92

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542.065 Million cell updates/sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	807	69.0	207	15	Sequence 76, Appl
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22	807	69.0	207	15	US-10-232-231-76	Sequence 76, Appl
23	807	69.0	207	15	US-10-232-233-76	Sequence 76, Appl
24	807	69.0	207	15	US-10-216-165-76	Sequence 76, Appl
25	807	69.0	207	15	US-10-218-956-76	Sequence 76, Appl
26	807	69.0	207	15	US-10-219-468-76	Sequence 76, Appl
27	807	69.0	207	15	US-10-219-478-76	Sequence 76, Appl
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ALIGNMENTS

RESULT 1
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; Patent No. US20020082388A1
; GENERAL INFORMATION:
; APPLICANT: Yue, Henry
; APPLICANT: Au-young, Janice
; APPLICANT: Patterson, Chandra
; TITLE OF INVENTION: CELL JUNCTION PDZ PROTEIN
; FILE REFERENCE: PF-0599 US
; CURRENT APPLICATION NUMBER: US/09/909,005
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/370,102
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1974337
US-09-909-005-1

Query Match	100.0%;	Score 1170;	DB 9;	Length 233;
Best Local Similarity	100.0%;	Pred. No. 1.4e-105;		
Matches 233;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MLKPSVTSAPTADMTLVVQPLTLDROVARAIELEKLOESGEVPHVKLSIKVQLQSE	60	
Db	1	MLKPSVTSAPTADMTLVVQPLTLDROVARAIELEKLOESGEVPHVKLSIKVQLQSE	60	
QY	61	FTATREYQYMHETITVNGCPFEFRARAKATAKATAFAASEGSHPRVVELPTDEGLGF	120	
Db	61	FTATREYQYMHETITVNGCPFEFRARAKATAKATAFAASEGSHPRVVELPTDEGLGF	120	
QY	121	NYMGKQNSPIYIRIIPGGVAERHGLRGDQLSVNGSVGEFHEKAYELLKAAD	180	

Db 121 NVMGKQNSPIYISRIIPGGVAERHGLKRGDQLLSVNGSVSEGEHHEKAVELLKAAKD 180
QY 181 SVKLVRVYTPKVLSEMEAREKLEKLTARRRQQQLLIQOQQOQQOQQOQQOQQOQQHMS 233
Db 181 SVKLVRVYTPKVLSEMEAREKLEKLTARRRQQQLLIQOQQOQQOQQOQQOQQOQQHMS 233

RESULT 2
US-10-216-163-76
; Sequence 76, Application US/10216163
; Publication No. US20030149239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerriitsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530F1C3
; CURRENT APPLICATION NUMBER: US/10/216,163
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089905
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25

Query Match 69.0%; Score 807; DB 12; Length 207;
Best Local Similarity 78.5%; Pred. No. 2.1e-70;
Matches 157; Conservative 24; Mismatches 17; Indels 2; Gaps 1;
QY 14 MATLTVQPLTLDKRDVARATLELLEKLOESGEPVPHKLSLKKVLSQSEFCTAIRREVYQYMH 73
Db 1 MAAL--VEPLGLEKRDVRAVELLRLQSRGELPPKQLQALQRLVLSQSFSAIRREVYPOLY 58
QY 74 ETITVNGCPPEPRARATKATVAFAASEGSHSPRVVLPKTDGELGNVGMGKQNSPIY 133
Db 59 DTLDTGSAETRAHATAKATVAATAEGHAHPRVVLPKTDGELGNVGMGKQNSPIY 118
QY 134 ISRIIPGGVAERHGLKRGDQLLSVNGSVSEGEHHEKAVELLKAAKDSVKLVVRYTPKVL 193
Db 119 ISRVIPGGVADRHGGLKRGDQLLSVNGSVSEGEHHEKAVELLKAAQGSVKLVVRYTPRVL 178
QY 194 EMEAREKLEKLTARRRQQQ 213

Db 179 EMEAREKLEKLTARRRQQQ 198

RESULT 3
US-10-227-884-76
; Sequence 76, Application US/10227884
; Publication No. US20030027988A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerriitsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530F1C79
; CURRENT APPLICATION NUMBER: US/10/227,884
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089905
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25

1 PRIOR APPLICATION NUMBER: 60/091982
2 PRIOR FILING DATE: 1998-07-07
3 PRIOR APPLICATION NUMBER: 60/095302
4 PRIOR FILING DATE: 1998-08-04
5 PRIOR APPLICATION NUMBER: 60/095318
6 PRIOR FILING DATE: 1998-08-04
7 PRIOR APPLICATION NUMBER: 60/095916
8 PRIOR FILING DATE: 1998-08-10
9 PRIOR APPLICATION NUMBER: 60/096146
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11 PRIOR APPLICATION NUMBER: 60/096791
12 PRIOR FILING DATE: 1998-08-17
13 PRIOR APPLICATION NUMBER: 60/097986
14 PRIOR FILING DATE: 1998-08-26
15 PRIOR APPLICATION NUMBER: 60/098544
16 PRIOR FILING DATE: 1998-08-31
17 PRIOR APPLICATION NUMBER: 60/099596
18 PRIOR FILING DATE: 1998-09-09
19 PRIOR APPLICATION NUMBER: 60/099598
20 PRIOR FILING DATE: 1998-09-09
21 PRIOR APPLICATION NUMBER: 60/099803
22 PRIOR FILING DATE: 1998-09-10
23 PRIOR APPLICATION NUMBER: 60/099811
24 PRIOR FILING DATE: 1998-09-10
25 PRIOR APPLICATION NUMBER: 60/099812
26 PRIOR FILING DATE: 1998-09-10
27 PRIOR APPLICATION NUMBER: 60/099816
28 PRIOR FILING DATE: 1998-09-10
29 PRIOR APPLICATION NUMBER: 60/100038
30 PRIOR FILING DATE: 1998-09-11
31 PRIOR APPLICATION NUMBER: 60/100385
32 PRIOR FILING DATE: 1998-09-15
33 PRIOR APPLICATION NUMBER: 60/100390
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35 PRIOR APPLICATION NUMBER: 60/100627
36 PRIOR FILING DATE: 1998-09-16
37 PRIOR APPLICATION NUMBER: 60/100848
38 PRIOR FILING DATE: 1998-09-18
39 PRIOR APPLICATION NUMBER: 60/100919
40 PRIOR FILING DATE: 1998-09-17
41 PRIOR APPLICATION NUMBER: 60/101477
42 PRIOR FILING DATE: 1998-09-23
43 PRIOR APPLICATION NUMBER: 60/101738
44 PRIOR FILING DATE: 1998-09-24
45 PRIOR APPLICATION NUMBER: 60/101741
46 PRIOR FILING DATE: 1998-09-24
47 PRIOR APPLICATION NUMBER: 60/101786
48 PRIOR FILING DATE: 1998-09-25
49 PRIOR APPLICATION NUMBER: 60/101916
50 PRIOR FILING DATE: 1998-09-24
51 PRIOR APPLICATION NUMBER: 60/101922
52 PRIOR FILING DATE: 1998-09-24
53 PRIOR APPLICATION NUMBER: 60/106178
54 PRIOR FILING DATE: 1998-10-28
55 PRIOR APPLICATION NUMBER: 60/106248
56 PRIOR FILING DATE: 1998-10-29
57 PRIOR APPLICATION NUMBER: 60/106464
58 PRIOR FILING DATE: 1998-10-30
59 PRIOR APPLICATION NUMBER: 60/106905
60 PRIOR FILING DATE: 1998-11-03
61 PRIOR APPLICATION NUMBER: 60/108787
62 PRIOR FILING DATE: 1998-11-17
63 PRIOR APPLICATION NUMBER: 60/108801
64 PRIOR FILING DATE: 1998-11-17
65 PRIOR APPLICATION NUMBER: 60/108849
66 PRIOR FILING DATE: 1998-11-18
67 PRIOR APPLICATION NUMBER: 60/112422
68 PRIOR FILING DATE: 1998-12-15
69 PRIOR APPLICATION NUMBER: 60/113296
70 PRIOR FILING DATE: 1998-12-22
71 PRIOR APPLICATION NUMBER: 60/113605
72 PRIOR FILING DATE: 1998-12-23
73 PRIOR APPLICATION NUMBER: 60/113621

1 PRIOR FILING DATE: 1998-12-23
2 PRIOR APPLICATION NUMBER: 60/115558
3 PRIOR FILING DATE: 1999-01-12
4 PRIOR APPLICATION NUMBER: 60/115565
5 PRIOR FILING DATE: 1999-01-12
6 PRIOR APPLICATION NUMBER: 60/115733
7 PRIOR FILING DATE: 1999-01-12
8 PRIOR APPLICATION NUMBER: 60/119549
9 PRIOR FILING DATE: 1999-02-10
10 PRIOR APPLICATION NUMBER: 60/123618
11 PRIOR FILING DATE: 1999-03-10
12 PRIOR APPLICATION NUMBER: 60/125259
13 PRIOR FILING DATE: 1999-03-19
14 PRIOR APPLICATION NUMBER: 60/125775
15 PRIOR FILING DATE: 1999-03-23
16 PRIOR APPLICATION NUMBER: 60/126773
17 PRIOR FILING DATE: 1999-03-29
18 PRIOR APPLICATION NUMBER: 60/127887
19 PRIOR FILING DATE: 1999-04-05
20 PRIOR APPLICATION NUMBER: 60/130232
21 PRIOR FILING DATE: 1999-04-21
22 PRIOR APPLICATION NUMBER: 60/131022
23 PRIOR FILING DATE: 1999-04-26
24 PRIOR APPLICATION NUMBER: 60/131270
25 PRIOR FILING DATE: 1999-04-27
26 PRIOR APPLICATION NUMBER: 60/131291
27 PRIOR FILING DATE: 1999-04-27
28 PRIOR APPLICATION NUMBER: 60/131445
29 PRIOR FILING DATE: 1999-04-28
30 PRIOR APPLICATION NUMBER: 60/134287
31 PRIOR FILING DATE: 1999-05-14
32 PRIOR APPLICATION NUMBER: 60/140650
33 PRIOR FILING DATE: 1999-06-22
34 PRIOR APPLICATION NUMBER: 60/140723
35 PRIOR FILING DATE: 1999-06-22
36 PRIOR APPLICATION NUMBER: 60/141037
37 PRIOR FILING DATE: 1999-06-23
38 PRIOR APPLICATION NUMBER: 60/144758
39 PRIOR FILING DATE: 1999-07-20
40 PRIOR APPLICATION NUMBER: 60/145698
41 PRIOR FILING DATE: 1999-07-26
42 PRIOR APPLICATION NUMBER: 60/146222
43 PRIOR FILING DATE: 1999-07-28
44 PRIOR APPLICATION NUMBER: 60/146963
45 PRIOR FILING DATE: 1999-08-03
46 PRIOR APPLICATION NUMBER: 60/149320
47 PRIOR FILING DATE: 1999-08-17
48 PRIOR APPLICATION NUMBER: 60/149638
49 PRIOR FILING DATE: 1999-08-17
50 PRIOR APPLICATION NUMBER: 60/151733
51 PRIOR FILING DATE: 1999-08-31
52 PRIOR APPLICATION NUMBER: 60/164418
53 PRIOR FILING DATE: 1999-11-09
54 PRIOR APPLICATION NUMBER: 60/166361
55 PRIOR FILING DATE: 1999-11-16
56 PRIOR APPLICATION NUMBER: 60/169445
57 PRIOR FILING DATE: 1999-12-07
58 PRIOR APPLICATION NUMBER: 60/169495
59 PRIOR FILING DATE: 1999-12-07
60 PRIOR APPLICATION NUMBER: 60/169835

Query Match 69.0%; Score 807; DB 15; Length 207;

Best Local Similarity 78.5%; Pred. No. 2.le-70;

Matches 157; Conservative 24; Mismatches 17; Indels 2; Gaps 1;

QY 14 MATLTVVQPLTLDRDVARAIELEKQESGEVPHVKLSKVLQSEFCTAIREVQYMH 73

Db 1 MAAL--VEPLGLERDVSRAVELLERLQSGELPPKQLQALQRLVQSRFCSAIREVVEQL 58

QY 74 ETTIVNGCPFRARATAKATVAFAASEGSHSPRVVELPKTDEGLGFNVMGKEQNSPIY 133

Db 59 DTLDITGSABIRAHATAKATVAFTASEGHAHPRVVELPKTDEGLGFNVMGKEQNSPIY 118

1 PRIOR APPLICATION NUMBER: 60/113296
2 PRIOR FILING DATE: 1998-12-22
3 PRIOR APPLICATION NUMBER: 60/113605
4 PRIOR FILING DATE: 1998-12-23
5 PRIOR APPLICATION NUMBER: 60/113621
6 PRIOR FILING DATE: 1998-12-23
7 PRIOR APPLICATION NUMBER: 60/115558
8 PRIOR FILING DATE: 1999-01-12
9 PRIOR APPLICATION NUMBER: 60/115565
10 PRIOR FILING DATE: 1999-01-12
11 PRIOR APPLICATION NUMBER: 60/115733
12 PRIOR FILING DATE: 1999-01-12
13 PRIOR APPLICATION NUMBER: 60/119549
14 PRIOR FILING DATE: 1999-02-10
15 PRIOR APPLICATION NUMBER: 60/123618
16 PRIOR FILING DATE: 1999-03-10
17 PRIOR APPLICATION NUMBER: 60/125259
18 PRIOR FILING DATE: 1999-03-19
19 PRIOR APPLICATION NUMBER: 60/125775
20 PRIOR FILING DATE: 1999-03-23
21 PRIOR APPLICATION NUMBER: 60/126773
22 PRIOR FILING DATE: 1999-03-29
23 PRIOR APPLICATION NUMBER: 60/127887
24 PRIOR FILING DATE: 1999-04-05
25 PRIOR APPLICATION NUMBER: 60/130232
26 PRIOR FILING DATE: 1999-04-21
27 PRIOR APPLICATION NUMBER: 60/131022
28 PRIOR FILING DATE: 1999-04-26
29 PRIOR APPLICATION NUMBER: 60/131270
30 PRIOR FILING DATE: 1999-04-27
31 PRIOR APPLICATION NUMBER: 60/131291
32 PRIOR FILING DATE: 1999-04-27
33 PRIOR APPLICATION NUMBER: 60/131445
34 PRIOR FILING DATE: 1999-04-28
35 PRIOR APPLICATION NUMBER: 60/134287
36 PRIOR FILING DATE: 1999-05-14
37 PRIOR APPLICATION NUMBER: 60/140650
38 PRIOR FILING DATE: 1999-06-22
39 PRIOR APPLICATION NUMBER: 60/140723
40 PRIOR FILING DATE: 1999-06-22
41 PRIOR APPLICATION NUMBER: 60/141037
42 PRIOR FILING DATE: 1999-06-23
43 PRIOR APPLICATION NUMBER: 60/144758
44 PRIOR FILING DATE: 1999-07-20
45 PRIOR APPLICATION NUMBER: 60/145698
46 PRIOR FILING DATE: 1999-07-26
47 PRIOR APPLICATION NUMBER: 60/146222
48 PRIOR FILING DATE: 1999-07-28
49 PRIOR APPLICATION NUMBER: 60/146963
50 PRIOR FILING DATE: 1999-08-03
51 PRIOR APPLICATION NUMBER: 60/149320
52 PRIOR FILING DATE: 1999-08-17
53 PRIOR APPLICATION NUMBER: 60/149638
54 PRIOR FILING DATE: 1999-08-17
55 PRIOR APPLICATION NUMBER: 60/151733
56 PRIOR FILING DATE: 1999-08-31
57 PRIOR APPLICATION NUMBER: 60/164418
58 PRIOR FILING DATE: 1999-11-09
59 PRIOR APPLICATION NUMBER: 60/166361
60 PRIOR FILING DATE: 1999-11-16
61 PRIOR APPLICATION NUMBER: 60/169445
62 PRIOR FILING DATE: 1999-12-07
63 PRIOR APPLICATION NUMBER: 60/169495
64 PRIOR FILING DATE: 1999-12-07
65 PRIOR APPLICATION NUMBER: 60/169835

Query Match 69.0%; Score 807; DB 15; Length 207;

Best Local Similarity 78.5%; Pred. No. 2.1e-70;

Matches 157; Conservative 24; Mismatches 17; Indels 2; Gaps 1;

14 MATLTVVQPLTLDROVARAIELEKLOESGEVPHVKLSKLVQSEFCTAIREVYQYMH 73

1 MAAL--VEPLGLERDVSRAVELLERLQSGELPPQKLQALQRLVQSRFCSAIREVYEQLY 58

QY

Db

74 ETITVNGCPEFRARATKATVAFAASEGHSHPRVVELPKTDGLGFNVNGKEQNSPIY 133
59 DTLDITGSAREIRAHATAKATVAFAASEGHSHPRVVELPKTDGLGFNVNGKEQNSPIY 118
134 ISRIIPGGVAERHGGGLKRGDQLLSVNGSVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVL 193
119 ISRVIPGGVADRHGGGLKRGDQLLSVNGSVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVL 178
194 EEMEARFEKLRTARRRQQQQ 213
179 EEMEARFEKMSARRRQQHQ 198

RESULT 5

US-10-149-819-19
; Sequence 19, Application US/10149819
; Publication No. US20030044913A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: YOE, Henry
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: TANG, Y. Tom
; APPLICANT: PATTERSON, Chandra
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LU, Dyung Aina M.
; APPLICANT: SHAH, Purvi
; APPLICANT: LAL, Preeti
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: BURFORD, Neil
; TITLE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
; FILE REFERENCE: PF-0760 PCT
; CURRENT APPLICATION NUMBER: US/10/149,819
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/172,852; 60/172,354
; PRIOR FILING DATE: 1999-12-10; 1999-12-16
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PERL Program
; SEQ ID NO 19
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No. US20030044913A1 4062841CDI
US-10-149-819-19

Query Match 69.0%; Score 807; DB 15; Length 207;
Best Local Similarity 78.5%; Pred. No. 2.1e-70;
Matches 157; Conservative 24; Mismatches 17; Indels 2; Gaps 1;

14 MATLTVVQPLTLDROVARAIELEKLOESGEVPHVKLSKLVQSEFCTAIREVYQYMH 73

1 MAAL--VEPLGLERDVSRAVELLERLQSGELPPQKLQALQRLVQSRFCSAIREVYEQLY 58

74 ETITVNGCPEFRARATKATVAFAASEGHSHPRVVELPKTDGLGFNVNGKEQNSPIY 133

59 DTLDITGSAREIRAHATAKATVAFAASEGHSHPRVVELPKTDGLGFNVNGKEQNSPIY 118

134 ISRIIPGGVAERHGGGLKRGDQLLSVNGSVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVL 193

119 ISRVIPGGVADRHGGGLKRGDQLLSVNGSVSVEGEHHEKAVELLKAAKDSVKLVVRYTPKVL 178

194 EEMEARFEKLRTARRRQQQQ 213

179 EEMEARFEKMSARRRQQHQ 198

RESULT 6

US-10-230-338-76

; Sequence 76, Application US/10230338

; Publication No. US20030044934A1

; GENERAL INFORMATION:


```
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C98
; CURRENT APPLICATION NUMBER: US/10/230,414
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 76
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-414-76

Query Match          69.0%; Score 807; DB 15; Length 207;
Best Local Similarity 78.5%; Pred. No. 2.1e-70;
Matches 157; Conservative 24; Mismatches 17; Indels 2; Gaps 1;

QY 14 MATITVQPLTDRDVARAIELKQLQSGEVPVHKLQSLKKVQLQSEFCTAIRVEYQYMH 73
Db 1 MAAL--VEPLGLERDVSRAVELLERLQSGELPQKQLQALQRLQSRFCSAIRVEYEQY 58
QY 74 ETIVVNGCPEPRARATKATVAFAASEGSHGHPRVVELPKTDGELGFNMGKQNSPIY 133
Db 59 DTLDITGSAETRAHATAKATVAFTAASEGHAHPRVVELPKTDGELGFNMGKQNSPIY 118
QY 134 ISRIIPGVVAERHGGKRGDOLLVNGSVSVEGEHKEKAVELLKAADSVKLVVRYTPKVL 193
Db 119 ISRVIPGVVADRHGGLKRGDOLLVNGSVSVEGEHKEKAVELLKAAGSVKLVVRYTPKVL 178
QY 194 EMEARFEKLTARRRQQQ 213
Db 179 EMEARFEKMSARRRQQHQ 198

RESULT 9
US-10-216-159A-76
; Sequence 76, Application US/10216159A
; Publication No. US20030069397A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C6
; CURRENT APPLICATION NUMBER: US/10/216,159A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 76
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-159A-76

Query Match          69.0%; Score 807; DB 15; Length 207;
Best Local Similarity 78.5%; Pred. No. 2.1e-70;
Matches 157; Conservative 24; Mismatches 17; Indels 2; Gaps 1;

QY 14 MATITVQPLTDRDVARAIELKQLQSGEVPVHKLQSLKKVQLQSEFCTAIRVEYQYMH 73
Db 1 MAAL--VEPLGLERDVSRAVELLERLQSGELPQKQLQALQRLQSRFCSAIRVEYEQY 58
QY 74 ETIVVNGCPEPRARATKATVAFAASEGSHGHPRVVELPKTDGELGFNMGKQNSPIY 133
Db 59 DTLDITGSAETRAHATAKATVAFTAASEGHAHPRVVELPKTDGELGFNMGKQNSPIY 118
QY 134 ISRIIPGVVAERHGGKRGDOLLVNGSVSVEGEHKEKAVELLKAADSVKLVVRYTPKVL 193
Db 119 ISRVIPGVVADRHGGLKRGDOLLVNGSVSVEGEHKEKAVELLKAAGSVKLVVRYTPKVL 178
QY 194 EMEARFEKLTARRRQQQ 213
Db 179 EMEARFEKMSARRRQQHQ 198

RESULT 10
US-10-218-849-76
; Sequence 76, Application US/10218849
; Publication No. US20030073814A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
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; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C11
; CURRENT APPLICATION NUMBER: US/10/218,849
; CURRENT FILING DATE: 2002-08-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 76
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-849-76

Query Match          69.0%; Score 807; DB 15; Length 207;
Best Local Similarity 78.5%; Pred. No. 2.le-70;
Matches 157; Conservative 24; Mismatches 17; Indels 2; Gaps 1;

QY 14 MATLVVQPLTDRVARAIELEKLEQSEGVPHKLOSKVKVLOSEFCTAIREVYQYMH 73
Db 1 MAAL--VEPLGLBRDVSRAVELLERLQSGELPPQKLQALQRYLQSFCAIREVYEQLY 58
QY 74 ETITVNGCPFRATATKATAFAAASEGHSHPRVVELPKTDGELGFNVMGKQNSPIY 133
Db 59 DILDITGSAIRAHATAKATAVAFTASEGHAHPRVVELPKTDGELGFNVMGKQNSPIY 118
QY 134 ISRIIPGGVAERGGKRGDQLLSVNGSVYEGHHEKAVELLKAADSKVLVRYTPKYL 193
Db 119 ISRVIPGGVADRGGKRGDQLLSVNGSVYEGHHEKAVELLKAADSKVLVRYTPRVL 178
QY 194 EEMEARFEKLRTARRRQQQ 213
Db 179 EEMEARFEKMRARRRQQHQ 198

RESULT 11
US-10-227-873-76
; Sequence 76, Application US/10227873
; Publication No. US20030073816A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C72
; CURRENT APPLICATION NUMBER: US/10/227,873
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
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;; PRIOR APPLICATION NUMBER: 60/101741
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101786
;; PRIOR FILING DATE: 1998-09-25
;; PRIOR APPLICATION NUMBER: 60/101916
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/101922
;; PRIOR FILING DATE: 1998-09-24
;; PRIOR APPLICATION NUMBER: 60/106178
;; PRIOR FILING DATE: 1998-10-28
;; PRIOR APPLICATION NUMBER: 60/106248
;; PRIOR FILING DATE: 1998-10-29
;; PRIOR APPLICATION NUMBER: 60/106464
;; PRIOR FILING DATE: 1998-10-30
;; PRIOR APPLICATION NUMBER: 60/106905
;; PRIOR FILING DATE: 1998-11-03
;; PRIOR APPLICATION NUMBER: 60/108787
;; PRIOR FILING DATE: 1998-11-17
;; PRIOR APPLICATION NUMBER: 60/108801
;; PRIOR FILING DATE: 1998-11-17
;; PRIOR APPLICATION NUMBER: 60/108849
;; PRIOR FILING DATE: 1998-11-18
;; PRIOR APPLICATION NUMBER: 60/112422
;; PRIOR FILING DATE: 1998-12-15
;; PRIOR APPLICATION NUMBER: 60/113296
;; PRIOR FILING DATE: 1998-12-22
;; PRIOR APPLICATION NUMBER: 60/113605
;; PRIOR FILING DATE: 1998-12-23
;; PRIOR APPLICATION NUMBER: 60/113621
;; PRIOR FILING DATE: 1998-12-23
;; PRIOR APPLICATION NUMBER: 60/115558
;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/115565
;; PRIOR FILING DATE: 1999-01-12
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;; PRIOR FILING DATE: 1999-01-12
;; PRIOR APPLICATION NUMBER: 60/119549
;; PRIOR FILING DATE: 1999-02-10
;; PRIOR APPLICATION NUMBER: 60/123618
;; PRIOR FILING DATE: 1999-03-10
;; PRIOR APPLICATION NUMBER: 60/125259
;; PRIOR FILING DATE: 1999-03-19
;; PRIOR APPLICATION NUMBER: 60/125775
;; PRIOR FILING DATE: 1999-03-23
;; PRIOR APPLICATION NUMBER: 60/126773
;; PRIOR FILING DATE: 1999-03-29
;; PRIOR APPLICATION NUMBER: 60/127887
;; PRIOR FILING DATE: 1999-04-05
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;; PRIOR FILING DATE: 1999-04-21
;; PRIOR APPLICATION NUMBER: 60/131022
;; PRIOR FILING DATE: 1999-04-26
;; PRIOR APPLICATION NUMBER: 60/131270
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;; PRIOR FILING DATE: 1999-04-27
;; PRIOR APPLICATION NUMBER: 60/131445
;; PRIOR FILING DATE: 1999-04-28
;; PRIOR APPLICATION NUMBER: 60/134287
;; PRIOR FILING DATE: 1999-05-14
;; PRIOR APPLICATION NUMBER: 60/140650
;; PRIOR FILING DATE: 1999-06-22
;; PRIOR APPLICATION NUMBER: 60/140723
;; PRIOR FILING DATE: 1999-06-22
;; PRIOR APPLICATION NUMBER: 60/141037
;; PRIOR FILING DATE: 1999-06-23
;; PRIOR APPLICATION NUMBER: 60/144758
;; PRIOR FILING DATE: 1999-07-20
;; PRIOR APPLICATION NUMBER: 60/145698
;; PRIOR FILING DATE: 1999-07-26
;; PRIOR APPLICATION NUMBER: 60/146222
;; PRIOR FILING DATE: 1999-07-28
;; PRIOR APPLICATION NUMBER: 60/146963

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;; PRIOR APPLICATION NUMBER: 60/149320
;; PRIOR FILING DATE: 1999-08-17
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;; PRIOR APPLICATION NUMBER: 60/151733
;; PRIOR FILING DATE: 1999-08-31
;; PRIOR APPLICATION NUMBER: 60/164418
;; PRIOR FILING DATE: 1999-11-09
;; PRIOR APPLICATION NUMBER: 60/166361
;; PRIOR FILING DATE: 1999-11-16
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;; PRIOR FILING DATE: 1999-12-07
;; PRIOR APPLICATION NUMBER: 60/169495
;; PRIOR FILING DATE: 1999-12-07
;; PRIOR APPLICATION NUMBER: 60/169835
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Best Local Similarity 78.5%; Pred. No. 2.1e-70;
Matches 157; Conservative 24; Mismatches 17; Indels 2; Gaps 1;
QY 14 MATLVVOPLTDRDVARATELEKQESGEPVHKLQSLKVLQSEFCTATREVVYMH 73
Db 1 MAAL--VEPLGLERDVSRAVELLERQSGELPPQKLQALQVLRQSFCSAIREVYEQLY 58
QY 74 ETIVNGCPFRARATATKATVAFAASEGSHSPRVVELPKTDGLGFNVMGKEQNSPIY 133
Db 59 DTLDTGSAIRAHATAKATVAFAASTEGHAHPRVVELPKTDGLGFNVMGKEQNSPIY 118
QY 134 ISRIIPGVAERHGGKRGDQLLSVNGSVSGEGHHEKAVELLKAAKDSVLYVRYTPKVL 193
Db 119 ISRVIPGVADRHGGKRGDQLLSVNGSVSGEGHHEKAVELLKAAKDSVLYVRYTPKVL 178
QY 194 EEMEARFEKLRTARRRQQQ 213
Db 179 EEMEARFEKMSARRRQQHQ 198
RESULT 12
US-10-227-883-76
; Sequence 76, Application US/10227883
; Publication No. US20030073817A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMERANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530PIC78
; CURRENT APPLICATION NUMBER: US/10/227,883
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Sequence
US-09-562-737-27

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Best Local Similarity 14.8%; Score 173.5; DB 4; Length 724;
Matches 37; Conservative 18; Mismatches 38; Indels 1; Gaps 1;

QY 106 PRVVELPTDGLGNVNGKQNSPIYISRIIPGGVAERHGGKRGDQLLSVNGSVSEG 165
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Db 311 PRRIVISRGSTGLGNTVGG-EDGEIVISILAGSPWDLSELKGYQLLSVNGVDARN 369
  ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 166 EHHEKAVELLKAADSVKLVVRYTPKYLEMEAR 199
  ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 370 ASHEQADALNAGQTVETIIAQYKPEEFSRFEAK 403
  ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||

RESULT 15
US-09-100-804-16
; Sequence 16, Application US/09100804
; Patent No. 6066472
; GENERAL INFORMATION:
; APPLICANT: GONEZ, LEONEL JORGE
; APPLICANT: SARAS, JAN
; APPLICANT: CLAESON-WELSH, LENA
; APPLICANT: HELDIN, CARL-HENRIK
; TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,804
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/596,291
; FILING DATE: 09-AUG-1996
; APPLICATION NUMBER: US 08/115,573
; FILING DATE: 01-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09943
; FILING DATE: 01-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: LO461/7003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 77 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEetical: NO
; ANTI-SENSE: NO
US-09-100-804-16
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Query Match
Best Local Similarity 14.7%; Score 172.5; DB 3; Length 77;
Matches 35; Conservative 16; Mismatches 19; Indels 3; Gaps 1;

QY 117 GLGFNVMGKQEQ---NSPIYISRIIPGGVAERHGGKRGDQLLSVNGSVSEGEHEKAVE 173
  ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 5 GLGFQIIGGERKMGRLDLGIFISSVAPGGPADFHGCLKPGDRLISVNSVSLGVSVSHAAIE 64
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QY 174 LKKAADSVKLVV 186
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Db 65 ILQNAPEDEVTLVI 77
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Search completed: September 23, 2003, 15:15:45
Job time : 20 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 23, 2003, 15:13:08 ; Search time 17 Seconds
(without alignments)
579.908 Million cell updates/sec

Title: US-09-909-005-1

Perfect score: 1170

Sequence: 1 MLKPSVTSAPTADMATLTVLLIQOQQOQQOQQOQQOQQNHS 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA: *
- 1: /cgn2.6/ptodata/1/1aa/5A_COMB.pep:*
 - 2: /cgn2.6/ptodata/1/1aa/5B_COMB.pep:*
 - 3: /cgn2.6/ptodata/1/1aa/6A_COMB.pep:*
 - 4: /cgn2.6/ptodata/1/1aa/6B_COMB.pep:*
 - 5: /cgn2.6/ptodata/1/1aa/PTCUS_COMB.pep:*
 - 6: /cgn2.6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1170	100.0	233	2	US-09-151-611-1
2	1170	100.0	233	3	US-09-370-102-1
3	643.5	55.0	297	2	US-09-151-611-3
4	643.5	55.0	297	3	US-09-370-102-3
5	196.5	16.8	724	4	US-09-562-737-21
6	190	16.2	1881	4	US-09-233-086-3
7	184	15.7	2465	2	US-08-596-291-3
8	184	15.7	2465	3	US-09-100-804-3
9	180.5	15.4	724	4	US-09-562-737-30
10	180.5	15.4	2466	3	US-09-080-855-12
11	180.5	15.4	2466	4	US-09-566-076-12
12	180.5	15.4	2466	5	PCT-US94-09943-2
13	174.5	14.9	2037	3	US-09-306-998-3
14	173.5	14.8	724	4	US-09-562-737-27
15	172.5	14.7	77	3	US-09-100-804-16
16	172.5	14.7	724	4	US-09-562-737-28
17	171	14.6	724	4	US-09-562-737-23
18	170.5	14.6	80	3	US-08-545-860D-54
19	170.5	14.6	80	5	PCT-US94-04496-54
20	169	14.4	2485	3	US-09-290-640-46
21	168.5	14.4	724	4	US-09-562-737-29
22	164.5	14.1	724	4	US-09-562-737-26
23	161.5	13.8	724	4	US-09-562-737-25
24	157.5	13.5	206	4	US-09-562-737-51
25	156.5	13.4	73	3	US-09-100-804-28
26	156.5	13.4	610	1	US-08-410-804-1
27	156.5	13.4	610	1	US-08-259-514-1

28 156.5 13.4 610 2 US-08-858-311-1 Sequence 1, Appli
29 155.5 13.3 73 3 US-09-100-804-25 Sequence 25, Appli
30 155 13.2 374 3 US-09-091-405-2 Sequence 25, Appli
31 155 13.2 631 4 US-09-147-119-7 Sequence 7, Appli
32 151.5 12.9 77 3 US-09-100-804-17 Sequence 17, Appli
33 149.5 12.8 724 4 US-09-562-737-24 Sequence 24, Appli
34 148.5 12.7 724 4 US-09-562-737-22 Sequence 22, Appli
35 148 12.6 632 4 US-09-996-243-219 Sequence 219, Appli
36 147.5 12.6 206 4 US-09-562-737-56 Sequence 56, Appli
37 147.5 12.6 505 1 US-08-123-161A-14 Sequence 14, Appli
38 147.5 12.6 505 1 US-08-483-278-14 Sequence 14, Appli
39 145.5 12.4 206 4 US-09-562-737-52 Sequence 52, Appli
40 145 12.4 358 4 US-09-740-027-4 Sequence 4, Appli
41 143.5 12.3 79 3 US-09-100-804-27 Sequence 27, Appli
42 143.5 12.3 86 3 US-08-545-860D-53 Sequence 53, Appli
43 143.5 12.3 86 5 PCT-US94-04496-53 Sequence 53, Appli
44 142.5 12.2 450 2 US-08-665-037-2 Sequence 2, Appli
45 142.5 12.2 450 2 US-08-666-067-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-151-611-1
; Sequence 1, Application US/09151611
; Patent No. 5958731
; GENERAL INFORMATION:
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Patterson, Chandra
; TITLE OF INVENTION: CELL JUNCTION PDZ PROTEIN
; FILE REFERENCE: PF-0599 US
; CURRENT APPLICATION NUMBER: US/09/151,611
; CURRENT FILING DATE: 1998-09-11
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 1974337
US-09-151-611-1

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Best Local Similarity 100.0%; Pred. No. 2.5e-109;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLKPSVTSAPTADMATLTVVQPLTLDKRDVARATLEKLEKESGVPVHKLSLKKVLOSE 60
Db 1 MLKPSVTSAPTADMATLTVVQPLTLDKRDVARATLEKLEKESGVPVHKLSLKKVLOSE 60
Qy 61 FCTAIREVYQYMHETITVNGCPEFRARATATVAFAASEGSHSPRVLPKTDGLGF 120
Db 61 FCTAIREVYQYMHETITVNGCPEFRARATATVAFAASEGSHSPRVLPKTDGLGF 120
Qy 121 NVMGKKONSPYISRIIPGVAERHGLKRGDOLLVNGSVSVEGEHEHKAVALLKAAD 180
Db 121 NVMGKKONSPYISRIIPGVAERHGLKRGDOLLVNGSVSVEGEHEHKAVALLKAAD 180
Qy 181 SVKLWRYTPKVLMEAREFEKLTARRRQQQLLIQOQQOQQOQQOQQNHS 233
Db 181 SVKLWRYTPKVLMEAREFEKLTARRRQQQLLIQOQQOQQOQQOQQNHS 233

RESULT 2
US-09-370-102-1
; Sequence 1, Application US/09370102
; Patent No. 6265547
; GENERAL INFORMATION:
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice

RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao X., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*."
RL Science 287:2185-2195(2000).
CC -!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
DR EMBL: AE003750; AAF56389.1;
DR HSP: Q12959; 1PDR.
DR FlyBase: FBgn039269; velli.
DR InterPro: IPR004172; L27.
DR InterPro: IPR004478; PDZ.
DR Pfam: PF02828; L27; 1.
DR Pfam: PF00595; PDZ; 1.
DR SMART: SM00569; L27; 1.
DR SMART: SM00228; PDZ; 1.
DR PROSITE: PS0106; PDZ; 1.
SQ SEQUENCE 195 AA; 21493 MW; EF9DF5ED71A73FBC CRC64;
Query Match 64.4%; Score 754; DB 5; Length 195;
Best Local Similarity 77.9%; Pred. No. 8.3e-54;
Matches 148; Conservative 20; Mismatches 22; Indels 0; Gaps 0;
QY 21 QPFLDRVARAIELLEKLOESGVPVHKVLSKVLQSEFCTAIREVYQVYMHETITVNG 80
DB 6 EPLTSLRSYDKRSIELLEKLOASGDPFTTKLAALOKVLNSDFMTSVREVYEHVETVDIQ 65
QY 81 CPEFRATATKATVAFAAASGHGHPRVVLPKPTDEGLGFGVNGKQNSPIYISRIIPG 140
DB 66 SHDVRSATATKATVAFAAASGHGHPRVVLPKPTDEGLGFGVNGKQNSPIYISRIIPG 125
QY 141 GVAERHGLKRGDQLLSVNGSVSGEHEHKAVELLKAOSVKLVRYTKVLEEMARF 200
DB 126 GVAERHGLKRGDQLLSVNGSVSGEHEHKAVELLKAOSVKLVRYTKVLEEMARF 185
QY 201 EKLRTARRQ 210
DB 186 DKQRTARRQ 195
RESULT 11
Q8INT8
ID Q8INT8 PRELIMINARY; PRT; 244 AA.
AC Q8INT8
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE CG7662-PB.
GN VELL.
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; *Drosophila*.
OX NCBI_taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Sutton G.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Taiton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Adayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.F., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Celnik S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Ranzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C.A., Nunoo J.,
RA Pacle J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirskaas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of *Drosophila melanogaster* genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celnik S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Krommiller B., Marshall B., Milburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of *Drosophila melanogaster* genome."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celnik S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE003750; AAN14038.1; --
SQ SEQUENCE 244 AA; 27467 MW; 0A464B355772A8A1 CRC64;
Query Match 58.5%; Score 684.5; DB 5; Length 244;
Best Local Similarity 59.8%; Pred. No. 5.2e-48;
Matches 144; Conservative 20; Mismatches 24; Indels 53; Gaps 2;
QY 21 QPFLDRVARAIELLEKLOESGVPVHKVLSKVLQSEFCTAIREVYQVYMHETITVNG 80
DB 6 EPLTSLRSYDKRSIELLEKLOASGDPFTTKLAALOKVLNSDFMTSVREVYEHVETVDIQ 65
QY 81 CPEFRATATKATVAFAAASGHGHPRVVLPKPTDEGLGFGVNGKQNSPIYISRIIPG 116
DB 66 SHDVRSATATKATVAFAAASGHGHPRVVLPKPTDEGLGFGVNGKQNSPIYISRIIPG 125

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QY 117 -----GLGFNMVGKQNSPIYISRIIPGGVAERHGL 149
Db 126 KYRPRIVSIHLTKALSIENFCSLGFNMVGKQNSPIYISRIIPGGVADRHGGL 185
QY 150 KRGDQLLSVNGSVGEHEKAVELLKAADSKVLVRYTPKVLSEMEARFEKLTARR 209
Db 186 KRGDQLLSVNG--VYRENHEKAVELLKQAVGSKVLVRYTPKVLSEMEARFEKLTARR 243
QY 210 Q 210
Db 244 Q 244

RESULT 12
ID 017458 PRELIMINARY; PRT: 171 AA.
AC 017458;
DT 01-JAN-1998 (TRENBLrel. 05, Created)
DT 01-JAN-1998 (TRENBLrel. 05, Last sequence update)
DE 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Hypothetical 19.0 kDa protein (Fragment).
OS Schistosoma mansoni (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6183;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Puerto Rican;
RX MEDLINE=99334538; PubMed=10406037;
RA Harrop R., Coulson P.S., Wilson R.A.;
RT "Characterization, cloning and immunogenicity of antigens released by
RT lung-stage larvae of Schistosoma mansoni.";
RL Parasitology 118:583-594(1999).
CC -!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
DR EMBL; AF030965; AAB86566.1; -.
DR HSP; P31016; IBEF.
DR InterPro; IPR004172; L27.
DR InterPro; IPR001478; PDZ.
DR Pfam; PF02828; L27; 1.
DR Pfam; PF00595; PDZ; 1.
DR SMART; SM00228; PDZ; 1.
DR PROSITE; PS0106; PDZ; 1.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 171 AA; 19000 MW; 69685F4108598063 CRC64;

Query Match 55.4%; Score 648.5; DB 5; Length 171;
Best Local Similarity 73.7%; Pred. No. 2.9e-45;
Matches 123; Conservative 26; Mismatches 17; Indels 1; Gaps 1;

QY 44 EYPVHKLSKLVQSECTAIREYQYMHETITVNGCPFRARAKATVAAPAAASGHH 103
Db 4 EIQPSKLAALQRIQLQSDFCMDIREYEHYITVDINGSEEVKASAKATVAAPAAASGHH 63
QY 104 SHPRVVELPKTDEGLGFNMVGKQNSPIYISRIIPGGVAERHGLKRGDQLLSVNGSV 163
Db 64 AHPRVIELPKTNEGLGFNMVGKQNSPIYISRXKPGGVADRHGGLKRGDQLLSVNGSV 123
QY 164 EGEHEKAVELLKAADSKVLVRYTPKVLSEMEARFEKLTARRQ 210
Db 124 ESEHERAVELLKLAQGTIVLVRYTPRILEMEARFDK-QKARRQ 169

RESULT 13
ID Q90245 PRELIMINARY; PRT: 316 AA.
AC Q90245;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)
DE 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Y54G11A.10 protein.
GN Y54G11A.10.

```

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OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RL Wallis J.M.;
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=98519116;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology.";
RC Science 282:2012-2018(1998).
CC -!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
DR EMBL; AL034488; CAA22459.2; -.
DR HSP; Q12959; IPDR.
DR WormPep; Y54G11A.10; CE28370.
DR InterPro; IPR004172; L27.
DR InterPro; IPR001478; PDZ.
DR Pfam; PF02828; L27; 1.
DR Pfam; PF00595; PDZ; 1.
DR SMART; SM00569; L27; 1.
DR SMART; SM00228; PDZ; 1.
DR PROSITE; PS0106; PDZ; 1.
DR PROSITE; PS0106; PDZ; 1.
SQ SEQUENCE 316 AA; 35663 MW; E050959F2D29BBFF CRC64;

Query Match 55.3%; Score 647.5; DB 5; Length 316;
Best Local Similarity 67.9%; Pred. No. 7.6e-45;
Matches 129; Conservative 30; Mismatches 30; Indels 1; Gaps 1;

QY 25 LDROVARAIELEKLOESGEVPHKLSKLVQSECTAIREYQYMHETITVNGCPFEF 84
Db 117 LERDYQRIELEMEHVQKTGEVNNAKLASLQVLOSEFFGAVREYETVYESIDADTTPEI 176
QY 85 RARATAKATVAFAASEGSHPRVVELPKTDEGLGFNMVGKQNSPIYISRIIPGGVAE 144
Db 177 KAATAKATVAFAAAGSHAPRIVELPKTDEGLGFNMVGKQNSPIYISRIIPGGVAD 236
QY 145 RHGGLKRGDQLLSVNGSVGEHEKAVELLKAADSKVLVRYTPKVLSEMEARFEKLR 204
Db 237 RHGGLKRGDQLIAVNG-NVEAECHKAVDLLKSAVGSVKLVIRYNPKLLDEMERFERQR 295
QY 205 TARRRQOQOL 214
Db 296 IRSTQOSPTL 305

RESULT 14
ID P90976 PRELIMINARY; PRT: 297 AA.
AC P90976;
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE LIN-7 (Fragment).
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96200771; PubMed=8612272;
RA Simske J.S., Kaech S.M., Harp S.A., Kim S.K.;
RT LET-23 receptor localization by the cell junction protein LIN-7
RT during C. elegans vulval induction.";
RL Cell 85:195-204(1996).
CC -!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
DR EMBL; U78092; AAB36684.1; -.
DR HSP; Q12959; IPDR.
DR InterPro; IPR004172; L27.
DR InterPro; IPR001478; PDZ.

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OM protein - protein search, using sw model

Run on: September 23, 2003, 15:11:58 ; Search time 37 seconds
(without alignments)
1625.034 Million cell updates/sec

Title: US-09-909-005-1
Perfect score: 1170
Sequence: 1 MLKPSVTSAPRADMATLTV.....LLIQQQQQQQQQQQQNHMS 233

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- SPTREMBL_23:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.priant:*
12: sp.virus:*
13: sp.vertibrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1170	100.0	233	4	O14910
2	1077.5	92.1	219	11	O92250
3	1057	90.3	211	11	O81ZS0
4	814	69.6	197	4	O9NUP9
5	814	69.6	197	11	O88952
6	809	69.1	207	11	O88951
7	809	69.1	207	11	O92252
8	807	69.0	207	4	O9HAP6
9	758	64.8	182	11	O92251
10	754	64.4	195	5	O9VEY7
11	684.5	58.5	244	5	O81MT8
12	648.5	55.4	171	5	O17458
13	647.5	55.3	316	5	O90245
14	643.5	55.0	297	5	P90976
15	233.5	20.0	967	5	O9B179
16	233.5	20.0	1064	5	O18165

17	219	18.7	852	11	O91XM9
18	208.5	17.8	960	5	O9VYZ4
19	208.5	17.8	968	5	O9VYZ5
20	199.5	17.1	403	11	O8BSV4
21	199.5	17.1	455	11	O920R1
22	199.5	17.1	455	11	O9ET11
23	199.5	17.1	463	11	O8BH60
24	198.5	17.0	454	4	O969U8
25	198.5	17.0	462	4	O9HD26
26	196.5	16.8	721	11	O91WJ1
27	192	16.4	893	11	O8CGN7
28	191.5	16.4	2055	11	O921K3
29	188.5	16.1	164	11	O8C0H8
30	187.5	16.0	526	11	O08783
31	187.5	16.0	2055	11	O8VBY0
32	187.5	16.0	2055	11	O8VBV5
33	187.5	16.0	2055	11	O8VBX6
34	186.5	15.9	2054	11	O55164
35	186	15.9	200	13	O90X35
36	185	15.8	927	11	O62402
37	178.5	15.3	526	11	O8K4T6
38	178.5	15.3	539	11	O8K4V4
39	177	15.1	1012	5	O21075
40	176.5	15.1	2484	6	O28006
41	176	15.0	513	5	O19846
42	173	15.0	531	5	O9W486
43	174.5	14.9	453	4	O43798
44	174.5	14.9	517	4	O8N790
45	174.5	14.9	582	4	O8WX31

ALIGNMENTS

RESULT 1

O14910 PRELIMINARY; PRT; 233 AA.
AC O14910:
DT 01-JAN-1998 (TREMELrel. 05, Created)
DT 01-MAY-1999 (TREMELrel. 10, Last sequence update)
DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
DE VELI 1 (TAX interaction protein 33) (Fragment).
GN MALS-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Testis;
RC MEDLINE=98424246; PubMed=9753324;
RX Butz S., Okamoto M., Sudhof T.C.;
FT "A tripartite protein complex with the potential to couple synaptic
vesicle exocytosis to cell adhesion in brain."
RL Cell 94:773-782(1998).
[2]
RN SEQUENCE OF 32-233 FROM N.A.
RA Roussel R., Fabre S., Desbois C., Bantignies F., Jalinot P.;
RL Oncogene 15:0-0(1997).
[3]
RN SEQUENCE FROM N.A.
RX MEDLINE=99274724; PubMed=10341223;
RA JO K., Derin R., Li M., Bredt D.S.;
FT "Characterization of MALS/Velis-1, -2, and -3: a family of mammalian
LIN-7 homologs enriched at brain synapses in association with the
postsynaptic density-95/NMDA receptor postsynaptic complex."
RL J. Neurosci. 19:4189-4199(1999).
CC -!- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
DR EMBL; AF087693; AAC78481.1; -
DR EMBL; AF028826; AAB84251.1; -
DR EMBL; AF173081; AAD48500.1; -
DR HSSP; Q12923; 3PDZ.
DR Genew; HGNC:17787; LIN7A.

AF028826

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OM protein - protein search, using sw model

Run on: September 23, 2003, 15:12:28 ; Search time 18 seconds
(without alignments)
1244.850 Million cell updates/sec

Title: US-09-909-005-1

Perfect score: 1170

Sequence: 1 MLKPSVTSAPTADMATLVV.....LLIQQQQQQQQQQQQQNHS 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	662	56.6	317	2 T27179	hypothetical prote
2	233.5	20.0	1131	2 T15617	hypothetical prote
3	219	18.7	852	2 T10811	channel associated
4	217.5	18.6	870	2 G01974	discs-large tumor
5	208.5	17.8	960	1 A39651	synapse-associated
6	196.5	16.8	720	2 A45436	postsynaptic densi
7	196.5	16.8	724	2 JH0800	postsynaptic densi
8	196.5	16.8	767	2 T09599	homolog of Drosoph
9	192	16.4	904	2 T38757	synapse-associated
10	192	16.4	911	2 T36552	homolog of Drosoph
11	192	16.4	926	2 T38736	multiple PDZ domai
12	191.5	16.4	2055	2 T30259	multi PDZ domain p
13	186.5	15.9	2054	2 T46612	hypothetical prote
14	177	15.1	1012	2 T23160	hypothetical prote
15	176	15.0	431	2 T16191	protein-tyrosine-p
16	173.5	14.8	2450	2 T16259	protein-tyrosine-p
17	172.5	14.7	2466	2 T16259	protein-tyrosine-p
18	169	14.4	2294	2 T16730	tyrosine phosphata
19	167.5	14.3	117	2 T181209	tyrosine phosphata
20	167.5	14.3	126	2 T42120	probable guanylate
21	165	14.1	1171	2 T42372	brain-specific ang
22	165	14.1	1256	2 J80209	protein-tyrosine-p
23	165	14.1	2490	1 A54971	atypical protein k
24	161	13.8	1337	2 T13948	hypothetical prote
25	159	13.6	578	2 T21345	hypothetical prote
26	154.5	13.2	390	2 T28036	hypothetical prote
27	154.5	13.2	423	2 T21570	hypothetical prote
28	154.5	13.2	440	2 T21568	hypothetical prote
29	151	12.9	538	2 T59291	betal-syntrophin -

30	151	12.9	628	2 T09458	numb-binding prote
31	151	12.9	728	2 T09457	numb-binding prote
32	151	12.9	1112	2 T32733	AMPA glutamate rec
33	151	12.9	1277	2 T14152	synaptic scaffold
34	150.5	12.9	87	2 S60315	PSD-95-related pro
35	147.5	12.6	488	2 T51379	svtrophin - Pacif
36	147.5	12.6	505	2 A53214	dystrophin-associa
37	146.5	12.5	503	2 T84771	dystrophin-1 - mou
38	145.5	12.4	505	2 S62894	alpha-syntrophin -
39	145.5	12.4	1893	2 A56158	eye development pr
40	144.5	12.4	450	2 G01158	tyrosine kinase ac
41	144.5	12.4	1281	2 T00346	hypothetical prote
42	142.5	12.2	358	2 T46532	protein co-factor
43	140.5	12.0	1095	2 T43275	neurabin - rat
44	138.5	11.8	2172	2 T20145	hypothetical prote
45	137.5	11.8	624	2 T19630	hypothetical prote

ALIGNMENTS

RESULT 1

T27179

Hypothetical protein Y54G11A.10 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T27179

R:Wallis, J.

submitted to the EMBL Data Library, December 1998

A:Reference number: Z20322

A:Accession: T27179

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-317 <WIL>

A:Cross-references: EMBL:AL034488; NID:el359895; PIDN:CAA22459.1; CESP:Y54G11A.10

A:Experimental source: clone Y54G11A

C:Genetics:

A:Gene: CESP:Y54G11A.10

A:Introns: 55/3; 108/3; 175/3; 228/2; 253/3

Query Match 56.6%; Score 662; DB 2; Length 317;

Best Local Similarity 68.4%; Pred. No. 2.5e-42;

Matches 130; Conservative 30; Mismatches 30; Indels 0; Gaps 0;

QY	25	LDROVARAIELEKLOESGEYVHKLSKLVLOSEFCTAIREVQYMHETITVNGCEPF	84
DB	117	LERDVRILELMEHVQKTGEVNNAKLASLQQLVSEFFGAVREYETVIESIDATTPEI	176
QY	85	RARATAKATVAFAASEGHSHPRVVELPKTDEGLGFNVMGKQNSPIYISRIIPGVAE	144
DB	177	KAATAKATVAFAAAEGHAHPRIVELPKTDQGLGFNVMGKQNSPIYISRIIPGVAD	236
QY	145	RHGGLKRGDQLLSVNGSVSEGEHHEKAVELKAAKDSVKLVVRYTPKVLMEARFEKL	204
DB	237	RHGGLKRGDQLIAYNGVNEAVEACHEKAVDLKSAVGSVKLVIRYMPKLLDEMERFER	296
QY	205	TARRRQQQL 214	
DB	297	IRSTQQSPTL 306	

RESULT 2

T15617

Hypothetical protein C25F6.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T15617

R:Bentley, D.

submitted to the EMBL Data Library, October 1995

A:Description: The sequence of C. elegans cosmid C25F6.

A:Reference number: T18377

A:Accession: T15617

A:Status: preliminary; translated from GB/EMBL/DBJ

C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jan-2000
C;Accession: I56552
R;Muller, B.M.; Kistner, U.; Veh, R.W.; Cases-Langhoff, C.; Becker, B.; Gundelfinger, E.
J. Neurosci. 15, 2354-2366, 1995
A;Title: Molecular characterization and spatial distribution of SAP97, a novel presynaptic protein.
A;Reference number: I56552; MUID:95198112; PMID:7891172
A;Accession: I56552
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-911 <RES>
C;Cross-references: EMBL:U14950; NID:9642455; PIDN:AAA79976.1; PID:9642456
C;Superfamily: discs-large tumor suppressor; GLGF domain homology; guanylate kinase homology
F;229-307/Domain: GLGF domain homology <GLG1>
F;323-401/Domain: GLGF domain homology <GLG2>
F;587-645/Domain: SH3 homology <SH3>
F;722-899/Domain: guanylate kinase homology <GKI>

Query Match 16.4%; Score 192; DB 2; Length 911;
Best Local Similarity 35.2%; Pred. No. 1.4e-06;
Matches 44; Conservative 23; Mismatches 44; Indels 14; Gaps 2;

QY 106 PRVVELPKTDEGLGFNVWGKEQNSPIYISRIIPGGVAERHGLKRGDQLLSVNGSVSEG 165
DB 106 PRVVELPKTDEGLGFNVWGKEQNSPIYISRIIPGGVAERHGLKRGDQLLSVNGSVSEG 165
DB 463 PRKVLHRRGSTGLGFNVVGG-EDGEGIFISFILLAGPADLSGELKRGDRIISVNSVDLRA 521
QY 166 EHHEKAVELLKAAKDSYKLVRYTPKYLEMEARFEKLR-----TARRRQOQ 212
DB 166 EHHEKAVELLKAAKDSYKLVRYTPKYLEMEARFEKLR-----TARRRQOQ 212
DB 522 ASHEQAAALKNAGQAVTIYVAQYRPEYSRFEAKIHLDRMTMNSVSSGSGSLRTSQKR 581
QY 213 QLLIQ 217
DB 582 SLYVR 586

RESULT 11
I38756
homology of Drosophila discs large protein, isoform 2 - human
C;Species: Homo sapiens (man)
C;Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jan-2000
C;Accession: I38756
R;Lue, R.A.; Marfatia, S.M.; Branton, D.; Chishti, A.H.
Proc. Natl. Acad. Sci. U.S.A. 91, 9818-9822, 1994
A;Title: Cloning and characterization of hdlg: the human homologue of the Drosophila discs large protein.
A;Reference number: I38756; MUID:95024052; PMID:7937897
A;Accession: I38756
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-926 <RES>
C;Cross-references: EMBL:U13896; NID:9558435; PIDN:AAA50598.1; PID:9558436
C;Genetics:
A;Gene: GDB:DLG1
A;Cross-references: GDB:393278; OMIM:601014
A;Map position: 3q29-3q29
C;Superfamily: discs-large tumor suppressor; GLGF domain homology; guanylate kinase homology
C;Keywords: alternative splicing; duplication
F;229-307/Domain: GLGF domain homology <GLG1>
F;324-402/Domain: GLGF domain homology <GLG2>
F;588-646/Domain: SH3 homology <SH3>
F;737-914/Domain: guanylate kinase homology <GKI>

Query Match 16.4%; Score 192; DB 2; Length 926;
Best Local Similarity 35.2%; Pred. No. 1.5e-06;
Matches 44; Conservative 23; Mismatches 44; Indels 14; Gaps 2;

QY 106 PRVVELPKTDEGLGFNVWGKEQNSPIYISRIIPGGVAERHGLKRGDQLLSVNGSVSEG 165
DB 106 PRVVELPKTDEGLGFNVWGKEQNSPIYISRIIPGGVAERHGLKRGDQLLSVNGSVSEG 165
DB 464 PRKVLHRRGSTGLGFNVVGG-EDGEGIFISFILLAGPADLSGELKRGDRIISVNSVDLRA 522
QY 166 EHHEKAVELLKAAKDSYKLVRYTPKYLEMEARFEKLR-----TARRRQOQ 212
DB 166 EHHEKAVELLKAAKDSYKLVRYTPKYLEMEARFEKLR-----TARRRQOQ 212
DB 523 ASHEQAAALKNAGQAVTIYVAQYRPEYSRFEAKIHLDRMTMNSVSSGSGSLRTSQKR 582

QY 213 QLLIQ 217
DB 583 SLYVR 587

RESULT 12
T30259
multiple PDZ domain protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C;Accession: T30259
R;Simpson, E.H.; Suffolk, R.; Jackson, I.J.
Genomics 59, 102-104, 1999
A;Title: Identification, sequence, and mapping of mouse multiple PDZ domain protein.
A;Reference number: Z20797; MUID:99326529; PMID:10395806
A;Accession: T30259
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-2055 <SIM>
A;Cross-references: EMBL:AJ131869; NID:94150877; PIDN:CAA10523.1; PID:94150878
A;Experimental source: strain C57/BL6 X CBA F1; whole brain
C;Genetics:
A;Gene: mpdz
A;Map position: 4

Query Match 16.4%; Score 191.5; DB 2; Length 2055;
Best Local Similarity 29.0%; Pred. No. 4.2e-06;
Matches 56; Conservative 31; Mismatches 81; Indels 25; Gaps 4;

QY 1 MLKPSVTSAPTADMAT----LTVVQPLTLDRDVARAIELEKLEQSEGVPHKLSLKKV 56
DB 1879 MHPNGVAAQTKLRVGDRIIVTCGTSTGDMTHQTQAVNLMKNASGSIEVQVAGGDVSV 1938
QY 57 LOSEFCTAREVYQYMHETITVNGCPPEFRARAKATAFAAASEGHSHPRVVELPKTDE 116
DB 1939 TG-----HQELANPCLAF-----TGLTSSSIFPDGLGPSQSKTTLDRGPD 1980
QY 117 GLGFNVWGG---KEQNSPIYISRIIPGGVAERHGLKRGDQLLSVNGSVSEGEHHEKAVE 173
DB 1981 GLSFNVVGGVSGPHGDLPIYVKVFAKGAADGRLKRGDIIIAVNGQSLEGVTHEEAVA 2040
QY 174 LLKAAKDSVKLVV 186
DB 2041 ILKRTKGTVTLMV 2053

RESULT 13
T46612
multi PDZ domain protein 1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 21-Jul-2000
C;Accession: T46612
R;Ullmer, C.; Schmuck, K.; Figge, A.; Lubbert, H.
FEBS Lett. 424, 63-68, 1998
A;Title: Cloning and characterization of MUPP1, a novel PDZ domain protein.
A;Reference number: Z23104; MUID:98196865; PMID:9537516
A;Accession: T46612
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-2054 <ULL>
A;Cross-references: EMBL:AJ001320; NID:92959978; PIDN:CAA04681.1; PID:92959979
A;Experimental source: brain
C;Genetics:
A;Gene: MUPP1

Query Match 15.9%; Score 186.5; DB 2; Length 2054;
Best Local Similarity 28.5%; Pred. No. 9.9e-06;
Matches 55; Conservative 31; Mismatches 82; Indels 25; Gaps 4;

QY 1 MLKPSVTSAPTADMAT----LTVVQPLTLDRDVARAIELEKLEQSEGVPHKLSLKKV 56
DB 1878 MHPNGVAAQTKLRVGDRIIVTCGTSTGDMTHQTQAVNLMKNASGSIEVQVAGGDVSV 1937

QY 57 LQSEFCTAIREVYOYMHETITVNGCPFRARATAKATVAFAASEGSHPRVPELPTKDE 116
Db 1938 TG-----HQEELANCLAF---TGLTSTTFPDDLGPQSKTITLDRGPD 1979
QY 117 GLGNVNGG---KQNSPIYISRIIPGVAERHGLKRGDQLLSVNGSVSVEGEHEKAVE 173
Db 1980 GLGFSIVGGYSGPHGLPIYVYKTFAKGAAEDGRLKRGDQIIAIVNGQSLEGVTHEEAVA 2039
QY 174 LLKAAKDSVKLVV 186
Db 2040 ILKRTGTGVTLMV 2052

RESULT 14
T23160
hypothetical protein K01A6.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Aug-2000
C:Accession: T23160
R:Cottage, A.
submitted to the EMBL Data Library, January 1996
A:Reference number: Z19701
A:Accession: T23160
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1012 <WIL>
A:Cross-references: EMBL:Z68750; PIDN:CAA92965.1; GSPDB:GNO00022; CESP:K01A6.1
A:Experimental source: clone K01A6
C:Genetics:
A:Gene: CESP:K01A6.1
A:Map position: 4
A:Introns: 107/1; 151/2; 183/2; 270/2; 316/3; 410/3; 628/3; 922/3; 971/3
C:Superfamily: WW repeat homology
F:131-168/Domain: WW repeat homology <WWR>

Query Match 15.1%; Score 177; DB 2; Length 1012;
Best Local Similarity 32.4%; Pred. No. 2.2e-05;
Matches 48; Conservative 30; Mismatches 50; Indels 20; Gaps 6;
QY 51 QSLKKVLQSEFCTAIREVYOYMHETITVNGCPFRARATAKATVAAPAA-----SEGHS 104
Db 620 QNVENTLQKQ--PAVTSEWEGMSAI-----PASMRPS--STTLGFATPNYIPLSQYNQ 670
QY 105 HPR---VVELPKTDEGLGFNVMGCKEQNSPIYISRIIPGVAERHGLKRGDQLLSVNGV 161
Db 671 KPSDLITVSLIRKPVGFRLLGVESKTPLSVGQIVIGAAEEDGRLQEGDEIVEIDGH 730
QY 162 SVEGEHEKAVELLKAAKDS--VKLVVR 187
Db 731 NVEGASHSEAVVLEAAAAQNKHVKLIVR 758

RESULT 15
T16191
hypothetical protein F27D9.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16191
R:Bentley, D.
submitted to the EMBL Data Library, February 1996
A:Description: The sequence of C. elegans cosmid F27D9.
A:Reference number: Z18473
A:Accession: T16191
A:Molecule type: DNA
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-431 <BEN>
A:Cross-references: EMBL:U49829; NID:g1203924; PID:g1203931; PIDN:AAA93388.1; CESP:F27D9.8
C:Genetics:
A:Gene: CESP:F27D9.8
A:Introns: 8/1; 52/3; 74/1; 96/1; 128/2; 149/3; 199/2; 255/3; 297/3; 319/3; 350/3; 390/3
Query Match 15.0%; Score 176; DB 2; Length 431;
Best Local Similarity 34.4%; Pred. No. 9.3e-06;

Matches 45; Conservative 26; Mismatches 46; Indels 14; Gaps 4;
QY 107 RVVELPKTDEGLGFNVMGCKE--QNSPIYISRIIPGVAERHGLKRGDQLLSVNGSVSVE 164
Db 36 QWIVKKPDSGFGLSIKGGSENAQNMPIVISKIFKGLPADCEGELFGIDAIVEYNGISIE 95
QY 165 GEHEKAVELLKAAKDSVKLVVR---TP-----KVLE---EMEAREFEKLTARRRQQ 212
Db 96 QSHDEVVNMCLKSSGDQYTLGVRFHTMTPLKPAQSLQPDGTLDDQLDFDGRSTRSHKAQS 155
QY 213 QLLIQQQQQQQ 223
Db 156 ESRLSDSKWQQ 166

Search completed: September 23, 2003, 15:15:21
Job time : 20 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 23, 2003, 15:11:13 : Search time 12 Seconds
(without alignments)
913.102 Million cell updates/sec

Title: US-09-909-005-1

Perfect score: 1170

Sequence: 1 MLKPSVTSAPADMAILTVV.....LLIQQQQQQQQQQQHMS 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 segs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	219	18.7	852	1	DLG2_RAT
2	217.5	18.6	870	1	DLG2_HUMAN
3	208.5	17.8	960	1	DLG1_DROME
4	203.5	17.4	817	1	DLG3_HUMAN
5	203.5	17.4	849	1	DLG3_MOUSE
6	203.5	17.4	849	1	DLG3_RAT
7	196.5	16.8	724	1	DLG4_MOUSE
8	196.5	16.8	724	1	DLG4_RAT
9	196.5	16.8	767	1	DLG4_HUMAN
10	192	16.4	904	1	DLG1_HUMAN
11	192	16.4	911	1	DLG1_RAT
12	169	14.4	2485	1	PTND_HUMAN
13	167	14.3	1356	1	DLG3_HUMAN
14	161.5	13.8	1333	1	PD3_MOUSE
15	161	13.7	1337	1	PD3_RAT
16	160	13.7	540	1	SNB2_HUMAN
17	158.5	13.5	520	1	SNB2_MOUSE
18	158	13.5	537	1	SNB1_MOUSE
19	158	13.5	637	1	MP4_HUMAN
20	157.5	13.5	206	1	STG2_RAT
21	157	13.4	539	1	STG2_HUMAN
22	155	13.2	631	1	IL16_HUMAN
23	152.5	13.0	145	1	SJ2B_HUMAN
24	152.5	13.0	910	1	US1C_MOUSE
25	151	12.9	538	1	SNB1_HUMAN
26	151	12.9	728	1	LNK1_MOUSE
27	148	12.6	539	1	STG2_MOUSE
28	148	12.6	728	1	LNK1_HUMAN
29	147.5	12.6	505	1	SNAL_RABIT
30	146.5	12.5	503	1	SNAL_MOUSE
31	145.5	12.4	505	1	SNAL_HUMAN
32	145.5	12.4	552	1	US1C_HUMAN
33	144.5	12.4	1809	1	DLG5_HUMAN

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34 143.5 12.3 742 1 NEB1_HUMAN
35 140.5 12.0 687 1 LNX2_MOUSE
36 140.5 12.0 1095 1 NEB1_RAT
37 137.5 11.8 1026 1 PTP1_CAEEL
38 137.5 11.8 1815 1 SHK3_RAT
39 137 11.7 1205 1 PA3L_HUMAN
40 136.5 11.7 690 1 LNX2_HUMAN
41 134 11.5 517 1 STG1_HUMAN
42 133 11.4 517 1 STG1_MOUSE
43 130.5 11.2 926 1 PTN4_HUMAN
44 129 11.0 553 1 MPP6_MOUSE
45 126.5 10.8 5038 1 PCLO_MOUSE

Q9uij8 homo sapien
Q9ixl2 mus musculus
O35867 rattus norv
P28191 caenorhabdi
Q9jlu4 rattus norv
Q8lew8 homo sapien
O8u448 homo sapien
Q9sn8 homo sapien
Q95el mus musculus
P29074 homo sapien
Q9jlb0 mus musculus
Q9gyx7 mus musculus

ALIGNMENTS

RESULT 1
DLG2_RAT STANDARD; PRT; 852 AA.
AC O63622; P70548; Q62939;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Channel associated protein of synapse-110 (Chapsyn-110) (Synaptic
DE density protein PSD-93) (Discs, large homolog 2).
GN DLG2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RP MEDLINE=96310881; PubMed=8755482;
RA Kim E., Cho K.O., Rothschild A., Sheng M.;
RT "Heteromultimerization and NMDA receptor-clustering activity of
RL Chapsyn-110, a member of the PSD-95 family of proteins.";
RN [2]
RP SEQUENCE FROM N.A.
RP MEDLINE=96193770; PubMed=8625413;
RA Brenman J.E., Chao D.S., Gee S.H., McGee A.W., Craven S.E.,
RA Santillano D.R., Wu Z., Huang F., Xia H., Peters M.F.,
RA Froehner S.C., Bredt D.S.;
RT "Interaction of nitric oxide synthase with the postsynaptic density
RL protein PSD-95 and alpha1-syntrophin mediated by PDZ domains.";
RN [3]
RP SEQUENCE FROM N.A.
RP Irie M., Hata Y., Takai Y.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF NMDA RECEPTOR
CC -!- SUBUNIT: AS WELL AS POTASSIUM CHANNELS.
CC -!- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
CC -!- SIMILARITY: Contains 3 PDZ/DHR domains.
CC -!- SIMILARITY: Contains 1 SH3 domain.
CC -!- SIMILARITY: Contains 1 guanylate kinase-like domain.
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CC -----
CC EMBL; U49049; AAB53243.1; -
CC EMBL; U50717; AAC52643.1; -
CC EMBL; U53368; AAB48562.1; -
CC PIR; T10811; T10811.
CC HSP; Q12959; IPDR.
CC InterPro; IPR000619; Guanylate_kin.
CC InterPro; IPR001478; PDZ.

```


ID DLG1_DROME STANDARD; PRT; 960 AA.
AC P31007;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Discs large-1 tumor suppressor protein.
GN DLG1 OR L(1)DLG1.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A., AND FUNCTION.
RC TISSUE=EMBRYO.
RX MEDLINE=91330294; PubMed=1651169;
RA Woods D.F., Bryant P.J.;
RT "The discs-large tumor suppressor gene of Drosophila encodes a
RL Cell 66:451-464(1991).
CC -!- FUNCTION: Plays a critical role at septate junctions in cellular
CC growth control during larval development. The presence of a
CC guanylate kinase domain suggests involvement in cellular adhesion
CC as well as signal transduction to control cellular proliferation.
CC Required for maintenance of cell polarity.
CC -!- SUBCELLULAR LOCATION: CYTOSKELETON-ASSOCIATED. LOCATED AT THE
CC CYTOPLASMIC FACE OF THE MEMBRANE IN THE CELLULAR BLASTODERM AND
CC BECOMES ASSOCIATED WITH SEPTATE JUNCTIONS WHICH BEGIN TO FORM
CC BETWEEN EPITHELIAL CELLS AT THE TIME OF DORSAL CLOSURE. IN ADULT
CC FLIES, LOCATED AT THE APICAL-LATERAL MEMBRANE BOUNDARY OF
CC EPITHELIAL CELLS.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing: Named isoforms=1;
CC Comment-A number of isoforms are produced;
CC Name=1;
CC IsoId=P31007-1; Sequence=Displayed;
CC -!- TISSUE SPECIFICITY: In embryos, expression is seen in epithelial
CC cells and some nervous tissue. In larvae, expression is seen as a
CC belt around salivary glands and imaginal disks, also in
CC proventriculus and parts of the brain. Expressed in adult
CC reproductive tissues. Expressed both maternally and zygotically
CC -!- DEVELOPMENTAL STAGE: Expressed both maternally and zygotically
CC throughout development.
CC -!- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
CC -!- SIMILARITY: Contains 3 PDZ/DHR domains.
CC -!- SIMILARITY: Contains 1 SH3 domain.
CC -!- SIMILARITY: Contains 1 guanylate kinase-like domain.
CC -----
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CC -----
DR EMBL; M73529; AAA28468.1;
DR PIR; A39651; A39651.
DR HSP; P31016; 1BFE.
DR FlyBase; FBgn0001624; dlgl.
DR GO; GO:0045179; C:apical cortex; IDA.
DR GO; GO:0016327; C:apicolateral plasma membrane; IDA.
DR GO; GO:0005918; C:septate junction; NAS.
DR GO; GO:0045175; P:basal protein localization; IMP.
DR GO; GO:0007391; P:dorsal closure; NAS.
DR GO; GO:0045197; P:establishment and/or maintenance of epithel. . . ; NAS.
DR GO; GO:0016334; P:establishment and/or maintenance of polarit. . . ; IGI.
DR GO; GO:0016336; P:establishment and/or maintenance of polarit. . . ; IGI.
DR GO; GO:0007399; P:neurogenesis; IMP.
DR GO; GO:0007273; P:regulation of synapse; IMP.
DR InterPro; IPR000619; Guanylate_kin.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR001452; SH3.

DR Pfam; PF00625; Guanylate_kin; 1.
DR Pfam; PF00595; PDZ; 3.
DR Pfam; PF00018; SH3; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00072; Gukc; 1.
DR SMART; SM00228; PDZ; 3.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00856; GUANYLATE_KINASE_1; 1.
DR PROSITE; PS0052; GUANYLATE_KINASE_2; 1.
DR PROSITE; PS0106; PDZ; 3.
DR PROSITE; PS0002; SH3; 1.
KW Transducer; SH3 domain; Alternative splicing; Repeat.
FT DOMAIN 40 126 PDZ 1.
FT DOMAIN 154 244 PDZ 2.
FT DOMAIN 486 566 PDZ 3.
FT DOMAIN 600 670 SH3.
FT DOMAIN 768 960 GUANYLATE_KINASE.
SQ SEQUENCE 960 AA; 102468 MW; BF87A4262F1B6AD5 CRC64;
Query Match 17.8%; Score 208.5; DB 1; Length 960;
Best Local Similarity 39.3%; Pred. No. 9.2e-08;
Matches 46; Conservative 21; Mismatches 49; Indels 1; Gaps 1;
QY 88 ATAKATVAFAAASEGSHPRVVELPKTDGLGFGNVMGKEQNSPIYISRIIPGGVAERHG 147
DB 466 AVPPCTPRAVSTEDITREPTTIQKPGGLGNIVGG-EDGGIVVSLAGGADLGS 524
QY 148 GUKRGDQLLSVNGSVSEGEHHEKAVELKAAKDSVKLVVYTPFKVLENEARPEKLR 204
DB 525 ELKRGDQLLSVNNVNLTHATHEEAQAALKTSGGVVTLAQYRPEYRPEARIQELK 581

RESULT 4

DLG3_HUMAN STANDARD; PRT; 817 AA.
ID DLG3_HUMAN
AC Q92796; Q9ULI8;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Presynaptic protein SAPI02 (Synapse-associated protein 102)
DE (Neuroendocrine-DLG) (NE-DLG) (Discs, large homolog 3).
GN DLG3 OR KIAA1232.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=97332623; PubMed=9188857;
RA Makino K., Kuwahara H., Masuko N., Nishiyama Y., Morisaki T.,
RA Sasaki J., Nakao M., Kuwano A., Nakata M., Ushio Y., Saya H.;
RT "Cloning and characterization of NE-dlg: a novel human homolog of the
RT Drosophila discs large (dlg) tumor suppressor protein interacts with
RT the APC protein.";
RL Oncogene 14:2425-2433(1997).
RN [2]
RP SEQUENCE OF 330-817 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20039619; PubMed=10574462;
RA Nagase T., Ishikawa K.-I., Kikuno R., Hirotsawa M., Nomura N.,
RA Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XV.
RT The complete sequences of 100 new cDNA clones from brain which code
RL for large proteins in vitro.";
RL DNA Res. 6:337-345(1999).
CC -!- FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF THE NMDA RECEPTOR
CC SUBUNIT NR2B (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
CC -!- SIMILARITY: Contains 3 PDZ/DHR domains.
CC -!- SIMILARITY: Contains 1 SH3 domain.
CC -!- SIMILARITY: Contains 1 guanylate kinase-like domain.
CC -----

MEDLINE=97432822; PubMed=9286702;
Stathakis D.G., Hoover K.B., You Z., Bryant P.J.;
"Human postsynaptic density-95 (PSD95): location of the gene (DLG4)
and possible function in nonneural as well as in neural tissues.";
Genomics 44:71-82(1997).
[2]
REVIEWS.
TISSUE=Mammary gland;
Stathakis D.G., Hoover K.H., You Z., Bryant P.J.;
Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
MEDLINE=20047407; PubMed=10582582;
Stathakis D.G., Odar N., Sandgren O., Andreasson S., Bryant P.J.,
Small K., Forsman-Semb K.;
"Genomic organization of human DLG4, the gene encoding postsynaptic
density 95.";
J. Neurochem. 73:2250-2265(1999).
[4]
SEQUENCE OF 81-401 FROM N.A.
TISSUE=Brain;
Brennan J.E., Bredt D.S., Parkinson J.F., Manzana W.P., McClary J.A.;
Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
[5]
INTERACTION WITH NLGN1; NLGN2 AND NLGN3.
PubMed=9278515;
Irie M., Hata Y., Takeuchi M., Ichchenko K., Toyoda A., Hirao K.,
Takai Y., Rosahl T.W., Suedhof T.C.;
"Binding of neuroligins to PSD-95";
Science 277:1511-1515(1997).
-!- FUNCTION: Interacts with the cytoplasmic tail of NMDA receptor
subunits. May be involved in synaptogenesis.
-!- SUBUNIT: Interacts with DLGAP1/GKAP (By similarity). Is part of a
complex with DLGAP1/GKAP, SHANK1, SHANK2 or SHANK3 (By similarity).
Binds to KIF13B. Interacts through its third PDZ domain with
NLGN1, and probably with NLGN2 and NLGN3.
-!- SUBCELLULAR LOCATION: Cytoplasmic. Concentrated at synaptic
junctions primarily on the presynaptic side. Also found in
postsynaptic density of neuronal cells (By similarity).
-!- TISSUE SPECIFICITY: BRAIN.
-!- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
-!- SIMILARITY: Contains 3 PDZ/DHR domains.
-!- SIMILARITY: Contains 1 SH3 domain.
-!- SIMILARITY: Contains 1 guanylate kinase-like domain.
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EMBL; U83192; AAC52113.1; -
EMBL; AF156495; AAD56173.1; -
EMBL; U68138; AAB07736.1; -
PIR; T09599; T09599.
PDB; 1KEF; 06-MAR-02.
Genew; HGNC:2903; DLG4.
MIM; 602887; -
GO; GO:0004384; F:membrane-associated guanylate kinase; TAS.
GO; GO:0008022; F:protein C-terminus binding activity; TAS.
GO; GO:0007612; P:learning; TAS.
GO; GO:0007399; P:neurogenesis; TAS.
GO; GO:0006461; P:protein complex assembly; TAS.
GO; GO:0007268; P:synaptic transmission; TAS.
InterPro; IPR000619; Guanylate_kin.
InterPro; IPR001478; PDZ.
InterPro; IPR001452; SH3.
Pfam; PF00625; Guanylate_kin; 1.
Pfam; PF00595; PDZ; 3.
Pfam; PF00018; SH3; 1.
ProDom; PD000066; SH3; 1.

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DR EMBL; UI3897; AAA50599.1; -
DR EMBL; UI3896; AAA50598.1; -
DR FIR; I38756; I38756.
DR PIR; I38757; I38757.
DR PDB; 1PDR; 23-JUL-97.
DR Genew; HGNC:2900; DLG1.
DR MIM; 601014; -
DR GO; GO:0005737; C:cytoplasm; TAS.
DR GO; GO:0005911; C:intercellular junction; TAS.
DR GO; GO:0003886; C:plasma membrane; TAS.
DR GO; GO:0008092; F:cytoskeletal protein binding activity; TAS.
DR GO; GO:0004385; F:guanylate kinase activity; TAS.
DR GO; GO:0004384; F:membrane-associated guanylate kinase; TAS.
DR GO; GO:0008181; F:tumor suppressor; TAS.
DR InterPro; IPR000619; Guanylate_kin.
DR InterPro; IPR004172; L27.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00625; Guanylate_kin; 1.
DR Pfam; PF00595; PDZ; 3.
DR Pfam; PF00018; SH3; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00072; GUKC; 1.
DR SMART; SM00569; L27; 1.
DR SMART; SM00228; PDZ; 3.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00856; GUANYLATE_KINASE_1; 1.
DR PROSITE; PS50052; GUANYLATE_KINASE_2; 1.
DR PROSITE; PS50106; PDZ; 3.
DR PROSITE; PS50002; SH3; 1.
KW SH3 domain; Repeat; Alternative splicing; 3D-structure.
FT DOMAIN 224 310 PDZ 1.
FT DOMAIN 319 405 PDZ 2.
FT DOMAIN 466 546 PDZ 3.
FT DOMAIN 581 651 SH3.
FT DOMAIN 714 904 SH3.
FT VARSPIC 669 680 GUANYLATE_KINASE.
FT EIPDDMGKGLK -> QSFNDKKKKNLFRKPKFFYKKNQDS
FT EQETSDAQQ (in isoform 2).
FT FTID-VSP_003150.

FT STRAND 465 470
FT STRAND 478 482
FT STRAND 489 494
FT TURN 496 497
FT HELIX 499 503
FT TURN 508 509
FT STRAND 510 515
FT TURN 516 517
FT STRAND 518 519
FT TURN 521 522
FT HELIX 525 533
FT TURN 534 534
FT STRAND 538 545
FT HELIX 547 554
SQ SEQUENCE 904 AA; 100354 MW; B78798D6BB0920D4 CRC64;

Query Match 16.4%; Score 192; DB 1; Length 904;
Best Local Similarity 35.2%; Pred. No. 1.4e-06;
Matches 44; Conservative 23; Mismatches 44; Indels 14; Gaps 2;

QY 106 PRVVELPKTDEGLCFNVMGKKEKNSPIYSRIIPGGVAERHGLKRGDQLLSVNGVSVEG 165
||| | : ||||| : ||| | : ||| | : ||| | : ||| | : ||| | :
DB 464 PRKVLHRSSTGLGFGNIVGG-EDGEGIFISFIAGGPADLSGLRKGDRISVNDLRA 522
||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | :
QY 166 EHEKAVELLKAADSKVLVRYTPKVLMEAREFEKLR-----TARRRQQQ 212
||| | : ||| | : ||| | : ||| | : ||| | : ||| | : ||| | :
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Db 523. ASHEQAAAALKNAGQAVTIVAQYRPEYSRFEAKIHLREOMMNSSISSGSGSLRTSQKR 582
QY 213 QLLIQ 217
Db 583 SLVVR 587
| ::
| ::

RESULT 11
DLG1_RAT
ID DLG1_RAT STANDARD; PRT; 911 AA.
AC Q62696;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Presynaptic protein SAP97 (Synapse-associated protein 97) (Discs,
DE large homolog 1).
GN DLG1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95198112; PubMed=7891172;
RA Mueller B.M., Kistner U., Veh R.W., Cases-Langhoff C., Becker B.,
RA Gundelfinger E.D., Garner C.C.;
RT "Molecular characterization and spatial distribution of SAP97, a
RT novel presynaptic protein homologous to SAP90 and the Drosophila
RT discs-large tumor suppressor protein.";
RL J. Neurosci. 15:2354-2366(1995).
CC -!- FUNCTION: INTERACTS WITH THE CYTOPLASMIC TAIL OF NMDA RECEPTOR
CC SUBUNITS. MAY BE INVOLVED IN SYNAPTOGENESIS. MAY PLAY A ROLE IN
CC CELL ADHESION.
CC -!- SUBCELLULAR LOCATION: IN CULTURED T84 CELLS, IT IS RESTRICTED TO
CC THE CYTOPLASMIC SURFACE OF THE PLASMA MEMBRANES BETWEEN ADJACENT
CC CELLS, BUT NOT AT THE EDGES OF CELLS LACKING CELL-CELL CONTACT.
CC -!- TISSUE SPECIFICITY: PRESYNAPTIC NERVE TERMINI OF EXCITATORY
CC SYNAPSES. IN OTHER BRAIN REGIONS, SAP97 IS FOUND IN AND ALONG
CC BUNDLES OF UNMYELINATED AXONS. SAP97 IS NOT RESTRICTED TO THE CNS,
CC BUT IS ALSO PRESENT AT THE BASAL LATERAL MEMBRANE BETWEEN A
CC VARIETY OF EPITHELIAL CELLS.
CC -!- SIMILARITY: BELONGS TO THE MAGUK FAMILY OF CELL JUNCTION PROTEINS.
CC -!- SIMILARITY: Contains 3 PDZ/DHR domains.
CC -!- SIMILARITY: Contains 1 SH3 domain.
CC -!- SIMILARITY: Contains 1 guanylate kinase-like domain.
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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DR PROSITE; PS50002; SH3; 1.
KW SH3 domain; Repeat.
FT DOMAIN 224 310 PDZ 1.
FT DOMAIN 318 404 PDZ 2.
FT DOMAIN 465 545 PDZ 3.
FT DOMAIN 580 650 SH3.
FT DOMAIN 721 911 GUANYLATE KINASE.
FT DOMAIN 527 530 POLY-ALA.
SQ SEQUENCE 911 AA; 100570 MW; 18CEBD31DD0CAF8B CRC64;

Query Match
Best Local Similarity 35.2%; Pred. No. 1.4e-06;
Matches 44; Conservative 23; Mismatches 44; Indels 14; Gaps 2;

QY 106 PRVVELPKTDEGIGENVMGSGKEQNSPIYISRIIPGVAERHGLKRGDQLLSVNGVSVEG 165
Db 463 PRKVLHRSSTGLGFNIVGG-EDGEGIFSIILAGGPADLSGELRGKDRILSIIVNSVDLRA 521
QY 166 EHHEKAVELLKAAKSDVKLYVRYTPKVLMEEMAEKFLR-----FARRRQQQ 212
Db 522 ASHEQAALAKNAGQAVTIQAQVPEYSRFEAKIHLDRETMNMNSVSSGGSGSLRTSQKR 581
QY 213 QLLIQ 217
Db 582 SLXVR 586

RESULT 12
PTND_HUMAN STANDARD; PRT; 2485 AA.
ID Q12923; Q15159; Q15263; Q15264; Q15265; Q16826;
AC 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 13 (EC 3.1.3.48)
DE (Protein-tyrosine phosphatase 1E) (PTP-El) (hPTP-El) (PTP-BAS)
DE phosphatase 1) (FAP-1).
DE PTPN13 OR PTPLE OR PTP11 OR PNP1.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SQ SEQUENCE FROM N.A.
RC TISSUE=Breast carcinoma;
RX MEDLINE=94350988; PubMed=8071359;
RA Banville D., Ahmad S., Stocco R., Shen S.-H.;
RT "A novel protein-tyrosine phosphatase with homology to both the
RT cytoskeletal proteins of the band 4.1 family and junction-associated
RT guanylate kinases.";
RL J. Biol. Chem. 269:22320-22327(1994).
RN [2]
SQ SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Leukemia;
RX MEDLINE=94116679; PubMed=8287977;
RA Maekawa K., Imagawa N., Nagamatsu M., Harada S.;
RT "Molecular cloning of a novel protein-tyrosine phosphatase containing
RT a membrane-binding domain and GLGF repeats.";
RL FEBS Lett. 337:200-206(1994).
RN [3]
SQ SEQUENCE FROM N.A.
RC TISSUE=Fibroblast;
RX MEDLINE=95014139; PubMed=7929060;
RA Saras J., Claesson-Welsh L., Heldin C.-H., Gonen L.J.;
RT "Cloning and characterization of PTP11, a protein tyrosine phosphatase
RT with similarities to cytoskeletal-associated proteins.";
RL J. Biol. Chem. 269:24082-24089(1994).
RN [4]
SQ SEQUENCE OF 1216-2490 FROM N.A.
RC TISSUE=Pancreas;
RA Wang H.Y.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.

RN INTERACTION WITH TRIP6.
RP MEDLINE=99329089; PubMed=10400701;
RA Murthy K.K., Clark K., Fortin Y., Shen S.-H., Banville D.;
RT "ZRP-1, a zyxin-related protein, interacts with the second PDZ domain
RT of the cytosolic protein tyrosine phosphatase hPTP1E.";
RL J. Biol. Chem. 274:20679-20687(1999).
RN [6]
SQ STRUCTURE BY NMR OF I361-1456.
RP MEDLINE=20170882; PubMed=10704206;
RA Kozlov G., Gehring K., Ekiel I.;
RT "Solution structure of the PDZ2 domain from human phosphatase hPTP1E
RT and its interactions with C-terminal peptides from the Fas
RT receptor.";
RL Biochemistry 39:2572-2580(2000).
CC -1- FUNCTION: BINDS TO A NEGATIVE REGULATORY DOMAIN IN FAS THAT
CC INHIBITS FAS-INDUCED APOPTOSIS.
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -1- SUBUNIT: Interacts with TRIP6 and Fas receptor through its second
CC PDZ domain.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=1;
CC IsoId=Q12923-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q12923-2; Sequence=VSP_000496;
CC Name=3;
CC IsoId=Q12923-3; Sequence=VSP_000497;
CC -1- TISSUE SPECIFICITY: PRESENT IN MOST TISSUES WITH THE EXCEPTION OF
CC THE LIVER AND SKELETAL MUSCLE. MOST ABUNDANT IN LUNG, KIDNEY AND
CC FETAL BRAIN.
CC -1- SIMILARITY: Contains 1 FERM domain.
CC -1- SIMILARITY: Contains 5 PDZ/DHR domains.
CC -1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY.
CC -----
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CC -----
CC EMBL; U12128; AAB60339.1; -
CC EMBL; D21209; BAA04750.1; -
CC EMBL; D21210; BAA04751.1; -
CC EMBL; D21211; BAA04752.1; -
CC EMBL; X80289; CAA56563.1; -
CC EMBL; X79676; CAA56124.1; -
CC PIR; A54971; A54971.
CC PIR; I67629; I67629.
CC PIR; I67630; I67630.
CC PDB; 3PDZ; 17-MAR-00.
CC PDB; 1D5G; 24-JUL-02.
CC Genew; HGNC:9646; PTPN13.
CC MIM; 600267; -
CC GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
CC InterPro; IPR000299; Band_4.1.
CC InterPro; IPR001478; PDZ.
CC InterPro; IPR000387; TYR_phosphatase.
CC InterPro; IPR000242; Tyr_PP.
CC Pfam; PF00373; Band_41; 1.
CC Pfam; PF00595; PDZ; 5.
CC Pfam; PF0102; Y_phosphatase; 1.
CC PRINTS; PR00935; BAND41.
CC PRINTS; PR00700; PTPPHPTASE.
CC SMART; SM00295; B41; 1.
CC SMART; SM00228; PDZ; 5.
CC SMART; SM00194; PTPC; 1.
CC PROSITE; PS00660; FERM_1; FALSE_NEG.
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DR PROSITE; PS00661; FERM_2; FALSE_NEG.
DR PROSITE; PS50057; FERM_3; 1.
DR PROSITE; PS50106; PDZ_5.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; FALSE_NEG.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW Structural protein; Cytoskeleton; Hydrolase; Repeat; 3D-structure;
KW Alternative splicing; Coiled coil.
FT DOMAIN 56 59 POLY-LEU.
FT DOMAIN 572 872 FERM.
FT DOMAIN 2237 2485 PROTEIN-TYROSINE PHOSPHATASE.
FT DOMAIN 379 399 COILED COIL (POTENTIAL).
FT DOMAIN 469 504 COILED COIL (POTENTIAL).
FT DOMAIN 1775 1804 COILED COIL (POTENTIAL).
FT DOMAIN 2057 2085 COILED COIL (POTENTIAL).
FT DOMAIN 1093 1178 PDZ 1.
FT DOMAIN 1368 1452 PDZ 2.
FT DOMAIN 1501 1588 PDZ 3.
FT DOMAIN 1788 1868 PDZ 4.
FT DOMAIN 1882 1965 PDZ 5.
FT DOMAIN 1742 1749 POLY-SER.
FT DOMAIN 2408 2408 BY SIMILARITY.
FT ACT_SITE 884 1074 Missing (in isoform 2).
FT VARSPPLIC 1056 1074 /FTID=VSP_000496.
FT VARSPPLIC 1134 1135 Missing (in isoform 3).
FT CONFLICT 1216 1229 /FTID=VSP_000497.
FT CONFLICT 1238 1239 KDHWSKGTLRHIS -> DLRSRSHCHVLAHL (IN REF. 4).
FT CONFLICT 1238 1239 GL -> A (IN REF. 4).
FT CONFLICT 1357 1357 S -> P (IN REF. 4).
FT CONFLICT 1362 1363 KP -> RS (IN REF. 4).
FT CONFLICT 1383 1383 T -> TVLFDK (IN REF. 1).
FT CONFLICT 1538 1538 P -> A (IN REF. 3).
FT CONFLICT 1649 1649 R -> K (IN REF. 4).
FT CONFLICT 1698 1714 KSEDRTICINFIYPKI -> RVKKIPFVPCFILRRK (IN REF. 4).
FT CONFLICT 1797 1797 G -> A (IN REF. 3).
FT CONFLICT 1856 1857 AA -> G (IN REF. 4).
FT CONFLICT 2069 2069 A -> S (IN REF. 4).
FT CONFLICT 2206 2210 GLLDQ -> VARS (IN REF. 4).
FT STRAND 1366 1371
FT TURN 1373 1375
FT STRAND 1380 1384
FT TURN 1387 1389
FT STRAND 1395 1400
FT TURN 1402 1403
FT STRAND 1405 1409
FT TURN 1410 1410
FT TURN 1414 1415
FT STRAND 1417 1418
FT STRAND 1420 1421
FT TURN 1422 1423
FT STRAND 1424 1425
FT HELIX 1431 1439
FT STRAND 1445 1450
SQ SEQUENCE 2485 AA; 276903 MW; 8D1B31597C66962B CRC64;

Query Match 14.4%; Score 169; DB 1; Length 2485;
Best Local Similarity 28.4%; Pred. No. 0.00022;
Matches 40; Conservative 26; Mismatches 43; Indels 32; Gaps 2;

QY 78 VNGCPFRARATKATVAFAAEGSHSPR-----V 108
Db 1309 ISDVTYDSRGDSMDENAYSSQDHTPKQESSSSVNTSKMNFYFSSPPKPGDIE 1368
QY 109 VELPKTDEGLGFNMVG---KEQNSPIYISRIIPGGVAERHGLKRGDQLLSVNGSVSEG 165
Db 1369 VELAKNDNSLGISVGTGVNTSVRHGIIYKAVIPOGAESDGRHKGDRVIAVNGVSLG 1428
QY 166 EHEKAVELLKAADSKLVW 186
Db 1429 ATHKQAVETLRNTGVVHLL 1449
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RESULT 13
PAD3_HUMAN
ID PAD3_HUMAN STANDARD; PRT; 1356 AA.
AC O8TEW0; O8TEW1; O8TEW2; O8TEW3; Q96K28; Q96RM6; Q96RM7; Q9BY57;
AC Q9BY58; Q9HC48; Q9NWL4; Q9NVE6;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Partitioning-defective 3 homolog (PARD-3) (PAR-3) (Atypical PKC
DE isotype-specific interacting protein) (ASIP) (CTCL tumor antigen se2-
DE 5).
OS PARD3 OR PAR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 3), AND INTERACTION WITH PARD6B.
RC TISSUE=Kidney;
RX MEDLINE=20394296; PubMed=10934474;
RA Joberty G., Petersen C., Gao L., Macara I.G.;
RT "The cell-polarity protein Par6 links Par3 and atypical protein kinase
RT C to Cdc42."
RL Nat. Cell Biol. 2:531-539(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 2; 3; 7; 8 AND 9).
RX PubMed=11642408;
RA Fang C.M., Xu Y.H.;
RT "Down-regulated expression of atypical PKC-binding domain deleted asip
RT isoforms in human hepatocellular carcinomas."
RL Cell Res. 11:223-229(2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5 AND 6), INTERACTION WITH
RP PARD6B AND PRKCG, AND TISSUE SPECIFICITY.
RX PubMed=12234671;
RA Gao L., Macara I.G., Joberty G.;
RT "Multiple splice variants of Par3 and of a novel related gene, Par3L,
RT produce proteins with different binding properties."
RL Gene 294:99-99(2002).
RN [4]
RP SEQUENCE OF 126-1356 FROM N.A. (ISOFORM 10).
RC TISSUE=Hepatoma, and Ovarian carcinoma;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
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